

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 11, 2005, 17:39:11 ; Search time 110.751 Seconds
(without alignments)
373.662 Million cell updates/sec

Title: US-10-054-873-6
Perfect score: 587
Sequence: 1 MFPTIPLSRFLFDNAMLRAHR.....IVEQCCTSICSPLYQLENYCN 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	587	100.0	107	2	AA42860	Aay42860 hGH-mini-
2	555.5	94.6	150	2	AA42861	Aay42861 Chimeric
3	315.5	53.7	116	2	AAR98897	Aar98897 SOD-proin
4	304	51.8	63	2	AAR68900	Aar68900 Human pro
5	304	51.8	117	2	AAR98896	Aar98896 SOD-proin
6	302.5	51.5	137	2	AAR71692	Aar71692 Mating fa
7	299	50.9	56	2	AAR68901	Aar68901 Human pro
8	299	50.9	56	2	AAR78665	Aar78665 Proinsuli
9	299	50.9	96	2	AAR68899	Aar68899 Human pro

10	299	50.9	96	2	AAR78662	Aar78662 Fusion pr
11	299	50.9	145	2	AAR71694	Aar71694 Mating fa
12	299	50.9	146	2	AAR71695	Aar71695 Mating fa
13	294	50.1	52	2	AAY42859	Aay42859 Human ins
14	293	49.9	57	2	AAR04582	Aar04582 Proinsuli
15	288.5	49.1	160	2	AAR79056	Aar79056 Glycosylp
16	287	48.9	52	2	AAR11899	Aar11899 Example o
17	287	48.9	65	2	AAW47365	Aaw47365 Preproins
18	287	48.9	138	2	AAR87086	Aar87086 pKV142 mo
19	286	48.7	667	7	ADF15065	Adf15065 Human alb
20	286	48.7	667	7	ADH21310	Adh21310 Human alb
21	285	48.6	116	8	ADM16551	Adm16551 Prepro-in
22	284.5	48.5	58	2	AAR96047	Aar96047 Modified
23	284.5	48.5	59	2	AAR96048	Aar96048 Modified
24	284.5	48.5	65	2	AAR88188	Aar88188 N-termina
25	284.5	48.5	109	1	AAP94645	Aap94645 Amino aci
26	284.5	48.5	123	2	AAW19240	Aaw19240 EEAEPK-MI
27	284.5	48.5	123	2	AAW69160	Aaw69160 DNA const
28	284.5	48.5	124	2	AAW78751	Aaw78751 pAK855 pr
29	284.5	48.5	124	6	ABP55059	Abp55059 Insulin p
30	284.5	48.5	124	6	ABB82578	Abb82578 Synthetic
31	284.5	48.5	125	2	AAW19242	Aaw19242 EEAEPK-MI
32	284	48.4	116	8	ADM16550	Adm16550 Prepro-in
33	284	48.4	138	1	AAP94643	Aap94643 Amino aci
34	284	48.4	138	2	AAW04890	Aaw04890 S. cerevi
35	284	48.4	140	2	AAR71693	Aar71693 Mating fa
36	284	48.4	140	2	AAR71690	Aar71690 Mating fa
37	284	48.4	671	7	ADF16490	Adf16490 Human alb
38	284	48.4	671	7	ADF16443	Adf16443 Human alb
39	284	48.4	671	7	ADH21765	Adh21765 Human alb
40	284	48.4	671	7	ADH21789	Adh21789 Human alb
41	283.5	48.3	53	2	AAR65883	Aar65883 Di-Arg-(B
42	283.5	48.3	53	2	AAW18007	Aaw18007 Ins1 doub
43	283.5	48.3	117	2	AAW78752	Aaw78752 Protein s
44	283.5	48.3	408	4	AAB30705	Aab30705 A Bacillu
45	283	48.2	667	7	ADF16445	Adf16445 Human alb

ALIGNMENTS

RESULT 1

AAY42860

ID AAY42860 standard; protein; 107 AA.

XX

AC AAY42860;

XX

DT 19-JAN-2000 (first entry)

XX

DE hGH-mini-proinsulin chimeric protein.

XX

KW Insulin; precursor; growth hormone; chaperone; intramolecular; folding;

KW conformation; chimeric protein; cleavable; recombinant; production;

KW yield.

XX

OS Synthetic.

OS Homo sapiens.

XX
 PN WO9950302-A1.
 XX
 PD 07-OCT-1999.
 XX
 PF 31-MAR-1998; 98WO-CN000052.
 XX
 PR 31-MAR-1998; 98WO-CN000052.
 XX
 PA (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LTD.
 XX
 PI Gan Z;
 XX
 DR WPI; 1999-610839/52.
 XX
 PT New chimeric proteins containing human growth hormone fragment, used
 PT particularly for the production of human insulin.
 XX
 PS Claim 13; Page 30; 46pp; English.
 XX
 CC This sequence represents a chimeric protein, hGH-mini-proinsulin. This
 CC chimeric protein contains an N-terminal fragment of human growth hormone
 CC (hGH) of the sequence given in AAY42855, a cleavable peptide linker
 CC (AAY42857), and a human insulin precursor comprising insulin A and B
 CC chains (AAY42859). The hGH portion of the chimeric protein acts as an
 CC intramolecular chaperone (IMC) for the insulin precursor, enabling it to
 CC fold correctly. The cleavable peptide linker has a C-terminal Arg residue
 CC which enables the hGH portion of the chimeric protein to be removed after
 CC folding has taken place. Production of recombinant human insulin via an
 CC hGH-proinsulin chimeric protein can provide human insulin with correctly
 CC linked cysteine bridges with fewer necessary procedural steps, and hence
 CC resulting in a higher yield of human insulin. The IMC sequences not only
 CC protect insulin sequences from intracellular degradation by a
 CC microorganism host, but also promote the folding of the fused insulin
 CC precursor, facilitate the solubility of the fusion protein and decrease
 CC the intermolecular interactions among the fusion proteins, thus allowing
 CC folding of the fused insulin precursor at commercially useful high
 CC concentrations. The procedural steps of cyanogen bromide cleavage,
 CC oxidative sulfitolysis and related purification steps can thus be
 CC eliminated, along with the use of high concentrations of mercaptan or the
 CC use of hydrophobic absorbent resins
 XX
 SQ Sequence 107 AA;

Query Match 100.0%; Score 587; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 3.2e-43;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFPTIPLSRLFDNAMLRAHRLHQLAFDITYQEFEEAYIPKEQKYSFLQNPLGTGPRFVNQH 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MFPTIPLSRLFDNAMLRAHRLHQLAFDITYQEFEEAYIPKEQKYSFLQNPLGTGPRFVNQH 60

 Qy 61 LCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 LCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107

RESULT 2

AAY42861

ID AAY42861 standard; protein; 150 AA.

XX

AC AAY42861;

XX

DT 19-JAN-2000 (first entry)

XX

DE Chimeric protein, SEQ ID 7.

XX

KW Insulin; precursor; growth hormone; chaperone; intramolecular; folding;
KW conformation; chimeric protein; cleavable; recombinant; production;
KW yield.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9950302-A1.

XX

PD 07-OCT-1999.

XX

PF 31-MAR-1998; 98WO-CN000052.

XX

PR 31-MAR-1998; 98WO-CN000052.

XX

PA (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LTD.

XX

PI Gan Z;

XX

DR WPI; 1999-610839/52.

XX

PT New chimeric proteins containing human growth hormone fragment, used
PT particularly for the production of human insulin.

XX

PS Claim 14; Page 30-31; 46pp; English.

XX

CC This sequence represents a chimeric protein, which contains an N-terminal
CC fragment of human growth hormone (hGH) of the sequence given in AAY42856,
CC a cleavable peptide linker (AAY42857), and a human insulin precursor
CC comprising insulin A and B chains (AAY42859). The hGH portion of the
CC chimeric protein acts as an intramolecular chaperone (IMC) for the
CC insulin precursor, enabling it to fold correctly. The cleavable peptide
CC linker has a C-terminal Arg residue which enables the hGH portion of the
CC chimeric protein to be removed after folding has taken place. Production
CC of recombinant human insulin via an hGH-proinsulin chimeric protein can
CC provide human insulin with correctly linked cysteine bridges with fewer
CC necessary procedural steps, and hence resulting in a higher yield of
CC human insulin. The IMC sequences not only protect insulin sequences from
CC intracellular degradation by a microorganism host, but also promote the
CC folding of the fused insulin precursor, facilitate the solubility of the
CC fusion protein and decrease the intermolecular interactions among the
CC commercially useful high concentrations. The procedural steps of cyanogen
CC bromide cleavage, oxidative sulfitolysis and related purification steps
CC can thus be eliminated, along with the use of high concentrations of
CC mercaptan or the use of hydrophobic absorbent resins

XX

SQ Sequence 150 AA;

Query Match 94.6%; Score 555.5; DB 2; Length 150;
Best Local Similarity 71.3%; Pred. No. 2.3e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

```
Qy      1 MFPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNP----- 49
          ||||||||||||||||||||||||||||||||||||||||||||
Db      1 MFPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIP 60

Qy     50 -----LGTGPRFVNQHLCGSHLVEALYLVCGER 77
          ||||||||||||||||||||||||||||||||||||||||
Db     61 TPSNREETQQKSNLELLRISLLLIQSWLEPVQLGTGPRFVNQHLCGSHLVEALYLVCGER 120

Qy     78 GFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
          ||||||||||||||||||||||||||||||||||||||||
Db    121 GFFYTPKTRGIVEQCCTSICSLYQLENYCN 150
```

RESULT 3

AAR98897

ID AAR98897 standard; protein; 116 AA.

XX

AC AAR98897;

XX

DT 03-FEB-1997 (first entry)

XX

DE SOD-proinsulin hybrid polypeptide.

XX

KW Insulin; proinsulin; hybrid polypeptide; protein folding;

KW enzymatic cleavage; cyanogen bromide; sulphitolysis.

XX

OS Homo sapiens.

XX

PN W09620724-A1.

XX

PD 11-JUL-1996.

XX

PF 29-DEC-1994; 94WO-US013268.

XX

PR 29-DEC-1994; 94WO-US013268.

XX

PA (BIOT-) BIO-TECHNOLOGY GENERAL CORP.

XX

PI Hartman JR, Mendelovitz S, Gorecki M;

XX

DR WPI; 1996-333766/33.

DR N-PSDB; AAT34670.

XX

PT Recombinant insulin prodn. by correctly folding pro-insulin hybrid

PT polypeptide - then enzymatic cleavage of folded product, does not require

PT sulphite protection of SH nor use of cyanogen bromide.

XX

PS Example 1B; Fig 7; 69pp; English.

XX

CC A new method for the production of recombinant human insulin comprises

CC folding a hybrid polypeptide comprising proinsulin under conditions that

CC permit correct disulphide bond formation and subjecting that folded
 CC protein to enzymatic cleavage. The insulin produced can then be purified.
 CC This sequence is a SOD-insulin B chain-Arg-insulin A chain hybrid
 CC polypeptide and is encoded by the plasmid construct pDBAST-LAT.
 CC Transformation of the proper E.coli host cells with pDBAST-LAT results in
 CC the efficient expression of the proinsulin hybrid polypeptide, useful for
 CC human insulin production. The method produces recombinant human insulin
 CC identical to the natural hormone. Hazardous and cumbersome procedures
 CC involving cyanogen bromide and sulphitolysis to protect SH groups are
 CC avoided since the entire hybrid polypeptide folds efficiently to the
 CC native structure even with the leader attached and Cys unprotected
 XX
 SQ Sequence 116 AA;

Query Match 53.7%; Score 315.5; DB 2; Length 116;
 Best Local Similarity 85.3%; Pred. No. 9.2e-20;
 Matches 58; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

Qy 43 YSFLQNPLGT---GPRFVNQHLGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSL 99
 : | | | : |||||
 Db 49 HEFGDNTAGSTSAGPRFVNQHLGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSL 108
 Qy 100 YQLENYCN 107
 |||||
 Db 109 YQLENYCN 116

RESULT 4

AAR68900

ID AAR68900 standard; peptide; 63 AA.

XX

AC AAR68900;

XX

DT 25-MAR-2003 (revised)

DT 02-MAR-1995 (first entry)

XX

DE Human pro-insulin 4.

XX

KW Pro-insulin; A-chain; B-chain; C-chain; disulphide; mercaptan;

KW chaotropic agent.

XX

OS Homo sapiens.

XX

PN EP600372-A1.

XX

PD 08-JUN-1994.

XX

PF 25-NOV-1993; 93EP-00118993.

XX

PR 02-DEC-1992; 92DE-04240420.

XX

PA (FARH) HOECHST AG.

XX

PI Obermeier R, Gerl M, Ludwig J, Sabel W;

XX

DR WPI; 1994-177718/22.

XX

DR WPI; 1996-333766/33.
 DR N-PSDB; AAT34669.
 XX
 PT Recombinant insulin prodn. by correctly folding pro-insulin hybrid
 PT polypeptide - then enzymatic cleavage of folded product, does not require
 PT sulphite protection of SH nor use of cyanogen bromide.
 XX
 PS Example 1A; Fig 6; 69pp; English.
 XX
 CC A new method for the production of recombinant human insulin comprises
 CC folding a hybrid polypeptide comprising proinsulin under conditions that
 CC permit correct disulphide bond formation and subjecting that folded
 CC protein to enzymatic cleavage. The insulin produced can then be purified.
 CC This sequence is a SOD-insulin B chain-Lys-Arg-insulin A chain hybrid
 CC polypeptide and is encoded by the plasmid construct pBAST-R.
 CC Transformation of the proper E.coli host cells with pBAST-R results in
 CC the efficient expression of the proinsulin hybrid polypeptide, useful for
 CC human insulin production. The method produces recombinant human insulin
 CC identical to the natural hormone. Hazardous and cumbersome procedures
 CC involving cyanogen bromide and sulphitolysis to protect SH groups are
 CC avoided since the entire hybrid polypeptide folds efficiently to the
 CC native structure even with the leader attached and Cys unprotected
 XX
 SQ Sequence 117 AA;

Query Match 51.8%; Score 304; DB 2; Length 117;
 Best Local Similarity 82.6%; Pred. No. 9.1e-19;
 Matches 57; Conservative 3; Mismatches 5; Indels 4; Gaps 2;

Qy 43 YSFLQNPLGT---GPRFVNQHLGSHLVEALYLVCGERGFFYTPKT-RGIVEQCCTSICS 98
 : | | | : |||||:|||||
 Db 49 HEFGDNTAGSTSAGPRFVNQHLGSHLIEALYLVCGERGFFYTPKTKRGIVEQCCTSICS 108
 Qy 99 LYQLENYCN 107
 |||||
 Db 109 LYQLENYCN 117

RESULT 6

AAR71692

ID AAR71692 standard; protein; 137 AA.

XX

AC AAR71692;

XX

DT 25-MAR-2003 (revised)

DT 20-NOV-1995 (first entry)

XX

DE Mating factor alpha 1-Insulin precursor ArgB31.

XX

KW Human insulin precursor ArgB31; diabetes; Zinc ion complex;
 KW mating factor alpha 1.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Protein 1. .85

FT /label= mating factor alpha-1

AC AAR68901;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-MAR-1995 (first entry)
 XX
 DE Human pro-insulin 3.
 XX
 KW Pro-insulin; A-chain; B-chain; C-chain; disulphide; mercaptan;
 KW chaotropic agent.
 XX
 OS Homo sapiens.
 XX
 PN EP600372-A1.
 XX
 PD 08-JUN-1994.
 XX
 PF 25-NOV-1993; 93EP-00118993.
 XX
 PR 02-DEC-1992; 92DE-04240420.
 XX
 PA (FARH) HOECHST AG.
 XX
 PI Obermeier R, Gerl M, Ludwig J, Sabel W;
 XX
 DR WPI; 1994-177718/22.
 XX
 PT Prodn. of pro-insulin with correct di:sulphide bridges - by treating
 PT recombinant precursor protein with mercaptan in alkali and in presence of
 PT chaotropic agent, then isolation on hydrophobic resin.
 XX
 PS Disclosure; Page 12; 15pp; German.
 XX
 CC Pro-insulin is produced by treating recombinant precursor protein with a
 CC mercaptan to provide 2-10 SH residues per Cys residue, in presence of a
 CC chaotropic agent and in aq. medium of pH 10-11, treating the prod. with 3
 CC -50 g hydrophobic adsorber resin per l aq. medium of pH 4-7, isolating
 CC the adsorbed resin and pro-insulin and desorbing the pro-insulin. This
 CC method produces pro-insulin with correctly bonded Cys bridges. Compared
 CC with known methods it involves fewer stages (esp. no sulphitolysis or
 CC cyanogen bromide cleavage) and overall losses during purification are
 CC reduced, i.e. the process is quicker and gives better yields. Sequences
 CC of insulin chain A, B and C are given in AAR68895-97. Sequences of pro-
 CC insulin 1-4 are given in AAR68898-901. (Updated on 25-MAR-2003 to correct
 CC PN field.)
 XX
 SQ Sequence 56 AA;

Query Match 50.9%; Score 299; DB 2; Length 56;
 Best Local Similarity 100.0%; Pred. No. 1.3e-18;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 56

RESULT 8

AAR78665

ID AAR78665 standard; protein; 56 AA.

XX

AC AAR78665;

XX

DT 03-APR-1996 (first entry)

XX

DE Proinsulin sequence 3.

XX

KW Proinsulin; post-translational modification; recombinant production;

KW protein folding; conformation.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Region 1. .4

FT /label= R2

FT /note= "a peptide of 4 amino acids"

FT Peptide 5. .34

FT /label= R1-(B2-B29)-Y

FT /note= "human insulin B-chain"

FT Region 35

FT /label= X

FT Peptide 36. .56

FT /label= Gly-(A2-A20)-R3

FT /note= "human insulin A-chain"

XX

PN EP668292-A2.

XX

PD 23-AUG-1995.

XX

PF 09-FEB-1995; 95EP-00101748.

XX

PR 18-FEB-1994; 94DE-04405179.

XX

PA (FARH) HOECHST AG.

XX

PI Obermeier R, Gerl M, Ludwig J, Sabel W;

XX

DR WPI; 1995-284754/38.

XX

PT Isolation of insulin that is correctly post-translationally processed -
PT by reacting pro:insulin with a mercaptan in the presence of a chaotropic
PT agent and purificn. after absorption to hydrophobic resin.

XX

PS Example 2; Page 13; 16pp; German.

XX

CC The present sequence is an example of a proinsulin molecule corresp. to
CC the general formula R2-R1-(B2-B29)-Y-X-Gly-(A2-A20)-R3 (II). In formula
CC (II), X = Lys, Arg or a peptide of 2-35 amino acids contg. Lys or Arg at
CC the N- and C-termini; Y = a natural amino acid; R1 = Phe or a bond; R2 =
CC H, Arg, Lys, a peptide of 2-45 amino acids contg. Arg or Lys at the N-
CC and C-termini; R3 = a natural amino acid; (A2-A20) and (B2-B29) are the
CC insulin A- and B-chain sequences from human or other insulin. The
CC proinsulin molecule (produced in recombinant E.coli) is reacted with
CC mercaptan at a ratio of 2-10 SH residues of mercaptan per Cys residue of
CC proinsulin. The reaction takes place in the presence of a chaotropic

CC method produces pro-insulin with correctly bonded Cys bridges. Compared
 CC with known methods it involves fewer stages (esp. no sulphitolysis or
 CC cyanogen bromide cleavage) and overall losses during purification are
 CC reduced, i.e. the process is quicker and gives better yields. Sequences
 CC of insulin chain A, B and C are given in AAR68895-97. Sequences of pro-
 CC insulin 1-4 are given in AAR68898-901. (Updated on 25-MAR-2003 to correct
 CC PN field.)

XX

SQ Sequence 96 AA;

Query Match 50.9%; Score 299; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 2.1e-18;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSI~~CS~~LYQLENYCN 107
 |||||
 Db 44 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSI~~CS~~LYQLENYCN 96

RESULT 10

AAR78662

ID AAR78662 standard; protein; 96 AA.

XX

AC AAR78662;

XX

DT 03-APR-1996 (first entry)

XX

DE Fusion protein contg. proinsulin sequence 3.

XX

KW Proinsulin; post-translational modification; recombinant production;
 KW protein folding; conformation.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Region 41. .44

FT /label= R2

FT /note= "a peptide of 4 amino acids"

FT Peptide 45. .74

FT /label= R1-(B2-B29)-Y

FT /note= "human insulin B-chain"

FT Region 75

FT /label= X

FT Peptide 76. .96

FT /label= Gly-(A2-A20)-R3

FT /note= "human insulin A-chain"

XX

PN EP668292-A2.

XX

PD 23-AUG-1995.

XX

PF 09-FEB-1995; 95EP-00101748.

XX

PR 18-FEB-1994; 94DE-04405179.

XX

PA (FARH) HOECHST AG.

XX

PI Obermeier R, Gerl M, Ludwig J, Sabel W;

XX

DR WPI; 1995-284754/38.

XX

PT Isolation of insulin that is correctly post-translationally processed -
PT by reacting pro:insulin with a mercaptan in the presence of a chaotropic
PT agent and purificn. after absorptio to hydrophobic resin.

XX

PS Example 2; Page 8; 16pp; German.

XX

CC The present sequence is that of a fusion protein, produced in E.coli
CC which contains an example of a proinsulin molecule corresp. to the
CC general formula R2-R1-(B2-B29)-Y-X-Gly-(A2-A20)-R3 (II). In formula (II),
CC X = Lys, Arg or a peptide of 2-35 amino acids contg. Lys or Arg at the N-
CC and C-termini; Y = a natural amino acid; R1 = Phe or a bond; R2 = H, Arg,
CC Lys, a peptide of 2-45 amino acids contg. Arg or Lys at the N- and C-
CC termini; R3 = a natural amino acid; (A2-A20) and (B2-B29) are the insulin
CC A- and B-chain sequences from human or other insulin. The proinsulin
CC molecule, released by cyanogen bromide, is reacted with mercaptan at a
CC ratio of 2-10 SH residues of mercaptan per Cys residue of proinsulin. The
CC reaction takes place in the presence of a chaotropic auxiliary agent at
CC pH 10-11 and results in proinsulin with correctly linked cystine bridges.
CC Reaction with trypsin and opt. carboxypeptidase B yields correctly folded
CC insulin. The insulin is isolated by absorptio on a hydrophobic resin

XX

SQ Sequence 96 AA;

Query Match 50.9%; Score 299; DB 2; Length 96;

Best Local Similarity 100.0%; Pred. No. 2.1e-18;

Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
|
Db 44 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 96

RESULT 11

AAR71694

ID AAR71694 standard; protein; 145 AA.

XX

AC AAR71694;

XX

DT 25-MAR-2003 (revised)

DT 20-NOV-1995 (first entry)

XX

DE Mating factor alpha 1-Insulin precursor ArgB1, ArgB31 N-terminal.

XX

KW Human insulin precursor ArgB1, ArgB31; diabetes; Zinc ion complex;
KW mating factor alpha 1; N-terminal EEAEAEAR.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Protein 1. .85

FT /label= mating factor alpha-1

FT Peptide 86. .93

FT /label= N-terminal peptide

FT Peptide 94. .124
 FT /label= B-chain
 FT Peptide 125. .145
 FT /label= A-chain
 XX
 PN WO9507931-A1.
 XX
 PD 23-MAR-1995.
 XX
 PF 16-SEP-1994; 94WO-DK000347.
 XX
 PR 17-SEP-1993; 93DK-00001044.
 PR 02-FEB-1994; 94US-00190829.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Havelund S, Halstrom JB, Jonassen I, Andersen AS, Markussen J;
 XX
 DR WPI; 1995-131314/17.
 DR N-PSDB; AAQ86429.
 XX
 PT Acylated insulin deriv. which may be present as a Zinc ion complex - is
 PT used to treat diabetes and is rapid acting.
 XX
 PS Example 5; Page 82-83; 100pp; English.
 XX
 CC AAQ86429 encodes AAR71694 mating factor alpha 1-Insulin precursor ArgB1,
 CC ArgB31 N-terminal EEAEAEAR. The insulin precursor comprises the B and A
 CC chains of a claimed human insulin derivative preceded by the N-terminal
 CC amino acids EEAEAEAR. In the final claimed compsn. they are covalently
 CC connected via disulphide bonds between Cys residues A7/B7 and A20/B19.
 CC The derivative, which may be present as a zinc ion complex, can be used
 CC as a fast action treatment for diabetes. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 145 AA;

Query Match 50.9%; Score 299; DB 2; Length 145;
 Best Local Similarity 100.0%; Pred. No. 3e-18;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 93 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 145

RESULT 12

AAR71695

ID AAR71695 standard; protein; 146 AA.

XX

AC AAR71695;

XX

DT 25-MAR-2003 (revised)

DT 20-NOV-1995 (first entry)

XX

DE Mating factor alpha 1-Insulin precursor ArgB1, ArgB31 N-terminal.

XX

KW Human insulin precursor ArgB1, ArgB31; diabetes; Zinc ion complex;
 KW mating factor alpha 1; N-terminal EEAEAEAER.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 1. .85
 FT /label= mating factor alpha-1
 FT Peptide 86. .94
 FT /label= N-terminal peptide
 FT Peptide 95. .125
 FT /label= B-chain
 FT Peptide 126. .146
 FT /label= A-chain
 XX
 PN WO9507931-A1.
 XX
 PD 23-MAR-1995.
 XX
 PF 16-SEP-1994; 94WO-DK000347.
 XX
 PR 17-SEP-1993; 93DK-00001044.
 PR 02-FEB-1994; 94US-00190829.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Havelund S, Halstrom JB, Jonassen I, Andersen AS, Markussen J;
 XX
 DR WPI; 1995-131314/17.
 DR N-PSDB; AAQ86432.
 XX
 PT Acylated insulin deriv. which may be present as a Zinc ion complex - is
 PT used to treat diabetes and is rapid acting.
 XX
 PS Example 6; Page 85; 100pp; English.
 XX
 CC AAQ86432 encodes AAR71695 mating factor alpha 1-Insulin precursor ArgB1,
 CC ArgB31 N-terminal EEAEAEAER. The insulin precursor comprises the B and A
 CC chains of a claimed human insulin derivative preceded by the N-terminal
 CC amino acids EEAEAEAER. In the final claimed compsn. they are covalently
 CC connected via disulphide bonds between Cys residues A7/B7 and A20/B19.
 CC The derivative, which may be present as a zinc ion complex, can be used
 CC as a fast action treatment for diabetes. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 146 AA;

Query Match 50.9%; Score 299; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 3e-18;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSIQSLYQLENYCN 107
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 94 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSIQSLYQLENYCN 146

RESULT 13

AA42859

ID AAY42859 standard; protein; 52 AA.

XX

AC AAY42859;

XX

DT 19-JAN-2000 (first entry)

XX

DE Human insulin precursor, SEQ ID 5.

XX

KW Insulin; precursor; growth hormone; chaperone; intramolecular; folding;
KW conformation; chimeric protein; cleavable; recombinant; production;
KW yield.

XX

OS Homo sapiens.

XX

PN WO9950302-A1.

XX

PD 07-OCT-1999.

XX

PF 31-MAR-1998; 98WO-CN000052.

XX

PR 31-MAR-1998; 98WO-CN000052.

XX

PA (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LTD.

XX

PI Gan Z;

XX

DR WPI; 1999-610839/52.

XX

PT New chimeric proteins containing human growth hormone fragment, used
PT particularly for the production of human insulin.

XX

PS Claim 12; Page 29-30; 46pp; English.

XX

CC This sequence represents a human insulin precursor comprising insulin A
CC and B chains. This insulin precursor is a component of the chimeric
CC proteins hGH-mini-proinsulin (AAY42860) and the chimeric protein given in
CC AAY42861. These chimeric proteins additionally contain an N-terminal
CC fragment of human growth hormone (hGH) and a cleavable peptide linker
CC (AAY42857). The hGH portion of the chimeric protein acts as an
CC intramolecular chaperone (IMC) for the insulin precursor, enabling it to
CC fold correctly. The cleavable peptide linker has a C-terminal Arg residue
CC which enables the hGH portion of the chimeric protein to be removed after
CC folding has taken place. Production of recombinant human insulin via an
CC hGH-proinsulin chimeric protein can provide human insulin with correctly
CC linked cysteine bridges with fewer necessary procedural steps, and hence
CC resulting in a higher yield of human insulin. The IMC sequences not only
CC protect insulin sequences from intracellular degradation by a
CC microorganism host, but also promote the folding of the fused insulin
CC precursor, facilitate the solubility of the fusion protein and decrease
CC the intermolecular interactions among the fusion proteins, thus allowing
CC folding of the fused insulin precursor at commercially useful high
CC concentrations. The procedural steps of cyanogen bromide cleavage,
CC oxidative sulfitolysis and related purification steps can thus be
CC eliminated, along with the use of high concentrations of mercaptan or the
CC use of hydrophobic absorbent resins

XX

SO Sequence 52 AA;

Query Match 50.1%; Score 294; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.2e-18;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSI~~CS~~LYQLENYCN 107
|||||

Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSI~~CS~~LYQLENYCN 52

RESULT 14

AAR04582

ID AAR04582 standard; protein; 57 AA.

XX

AC AAR04582;

XX

DT 09-SEP-2004 (revised)

DT 25-MAR-2003 (revised)

DT 14-SEP-1990 (first entry)

XX

DE Proinsulin analogue with a Lys residue linking the A and B chains.

XX

KW insulin fusion protein; pro-insulin analogue; tendamistate;

KW Lys-Lys bridge; ds.

XX

OS Synthetic.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Peptide	1. .35
----	---------	--------

```

FT      /note= "Insulin B chain"

```

FT Misc-difference 36

```
FT      /note= "Lys residue linking insulin B chain to A chain"
```

FT	Peptide	37. .57
----	---------	---------

```
FT      /note= "Insulin A chain"
```

XX

PN EP367163-A.

XX

PD 09-MAY-1990.

XX

PF 28-OCT-1989; 89EP-00120056.

XX

PR 03-NOV-1988; 88DE-03837273.

PR 19-AUG-1989; 89DE-03927449.

XX

PA (FARH) HOECHST AG.

XX

PI Koller KP, Riess GJ, Uhlmann E, Wallmeier H;

XX

DR WPI; 1990-141149/19.

DR N-PSDB; AAQ04335.

XX

PT New insulin fusion proteins - comprise pro-insulin analogue linked to

PT tendamistate.

XX

PS Disclosure; Page 5; 8pp; German.

XX

CC This sequence is joined to the C-terminus of an N-terminal fragment
CC comprising opt. modified tendamistate. This fusion protein may be
CC converted into human insulin using known methods. The synthetic gene was
CC prepared by the phosphoramidite method. See also AAQ04336. (Updated on 25
CC -MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI
CC field.)
CC
CC Revised record issued on 09-SEP-2004 : Correction to pages and features
XX
SQ Sequence 57 AA;

RESULT 15
AAR79056

OM protein - protein search, using sw model

Run on: February 11, 2005, 18:04:56 ; Search time 28.2306 Seconds
(without alignments)
282.936 Million cell updates/sec

Title: US-10-054-873-6
Perfect score: 587
Sequence: 1 MFPTIPLSRLFDNAMLRAHR.....IVEQCCTSICSLYQLENYCN 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query		DB	ID	Description
	Score	Match	Length				
1	304	51.8	63	1	US-08-160-376A-6	Sequence 6, Appli	
2	302.5	51.5	137	1	US-08-400-256-39	Sequence 39, Appl	
3	302.5	51.5	137	3	US-08-975-365-39	Sequence 39, Appl	
4	299.5	51.0	66	1	US-08-291-060B-5	Sequence 5, Appli	
5	299	50.9	56	1	US-08-160-376A-7	Sequence 7, Appli	
6	299	50.9	56	1	US-08-389-487-11	Sequence 11, Appl	
7	299	50.9	96	1	US-08-160-376A-5	Sequence 5, Appli	
8	299	50.9	96	1	US-08-389-487-8	Sequence 8, Appli	
9	299	50.9	145	1	US-08-400-256-45	Sequence 45, Appl	
10	299	50.9	145	3	US-08-975-365-45	Sequence 45, Appl	
11	299	50.9	146	1	US-08-400-256-48	Sequence 48, Appl	

12	299	50.9	146	3	US-08-975-365-48	Sequence 48, Appl
13	293	49.9	57	1	US-08-030-731A-44	Sequence 44, Appl
14	287	48.9	65	3	US-08-900-574-3	Sequence 3, Appli
15	286.5	48.8	66	3	US-08-900-574-5	Sequence 5, Appli
16	286	48.7	67	3	US-08-900-574-7	Sequence 7, Appli
17	284.5	48.5	65	1	US-08-468-674B-71	Sequence 71, Appl
18	284.5	48.5	65	1	US-08-780-571-71	Sequence 71, Appl
19	284.5	48.5	124	3	US-09-012-669F-36	Sequence 36, Appl
20	284.5	48.5	124	4	US-09-894-711-18	Sequence 18, Appl
21	284	48.4	138	3	US-08-932-082-19	Sequence 19, Appl
22	284	48.4	138	4	US-09-861-687-19	Sequence 19, Appl
23	284	48.4	140	1	US-08-400-256-33	Sequence 33, Appl
24	284	48.4	140	1	US-08-400-256-42	Sequence 42, Appl
25	284	48.4	140	3	US-08-975-365-33	Sequence 33, Appl
26	284	48.4	140	3	US-08-975-365-42	Sequence 42, Appl
27	283.5	48.3	53	1	US-08-233-617-4	Sequence 4, Appli
28	283.5	48.3	53	3	US-08-981-988A-42	Sequence 42, Appl
29	283.5	48.3	117	3	US-09-012-669F-37	Sequence 37, Appl
30	281	47.9	104	1	US-08-400-256-15	Sequence 15, Appl
31	281	47.9	104	3	US-08-975-365-15	Sequence 15, Appl
32	280.5	47.8	89	1	US-08-468-674B-41	Sequence 41, Appl
33	280.5	47.8	89	1	US-08-780-571-41	Sequence 41, Appl
34	280.5	47.8	91	1	US-08-468-674B-45	Sequence 45, Appl
35	280.5	47.8	91	1	US-08-780-571-45	Sequence 45, Appl
36	280.5	47.8	124	1	US-08-446-646-3	Sequence 3, Appli
37	279.5	47.6	167	1	US-07-918-953-8	Sequence 8, Appli
38	279.5	47.6	167	1	US-08-081-661-8	Sequence 8, Appli
39	278.5	47.4	51	4	US-09-477-924-3	Sequence 3, Appli
40	278.5	47.4	51	4	US-09-723-981-3	Sequence 3, Appli
41	278.5	47.4	51	4	US-09-723-896-3	Sequence 3, Appli
42	278	47.4	117	4	US-09-280-030-63	Sequence 63, Appl
43	277.5	47.3	53	1	US-08-233-617-3	Sequence 3, Appli
44	277	47.2	96	2	US-09-134-836-4	Sequence 4, Appli
45	277	47.2	96	3	US-09-386-303A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-08-160-376A-6

; Sequence 6, Application US/08160376A

; Patent No. 5473049

; GENERAL INFORMATION:

; APPLICANT: Obermeier, Ranier

; APPLICANT: Gerl, Martin

; APPLICANT: Ludwig, Jorgen

; APPLICANT: Sabel, Walter

; TITLE OF INVENTION: Process For Obtaining Proinsulin

; TITLE OF INVENTION: Possessing Correctly Linked

; TITLE OF INVENTION: Cystine Bridges

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kenneth A. Genoni, Esq.

; STREET: Rt. 202-206 No. 5473049th/P.O. Box 2500

; CITY: Somerville

; STATE: New Jersey


```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/400,256
; FILING DATE: 03-MAR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3985.220-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-400-256-39

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Query Match          51.5%; Score 302.5; DB 1; Length 137;
Best Local Similarity 50.0%; Pred. No. 4.6e-28;
Matches 70; Conservative 4; Mismatches 27; Indels 39; Gaps 4;

```

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Qy      2 FPTIPLSRFLDNAMLRAHRLHQLAFDITYQEFEEAYIPKEQ--KYSFLQ-----N 48
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Db      3 FPSI-----FTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVLPSN 57

Qy      49 PLGTG-----PRFVNQHLCGSHLVEALYLVCGERGFFYTPKTRG 87
      |
Db      58 STNNGLLFINTTIIASIAAKEEGVSMKRFVNQHLCGSHLVEALYLVCGERGFFYTPKTRG 117

Qy      88 IVEQCCTSICSLYQLENYCN 107
      |||||
Db      118 IVEQCCTSICSLYQLENYCN 137

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RESULT 3

US-08-975-365-39

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; Sequence 39, Application US/08975365
; Patent No. 6011007
; GENERAL INFORMATION:
; APPLICANT: Havelund, Svend
; APPLICANT: Halstrom, John
; APPLICANT: Jonassen, Ib
; APPLICANT: Andersen, Asser Sloth
; APPLICANT: Markussen, Jan
; TITLE OF INVENTION: ACYLATED INSULIN
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6011007o No. 6011007disk of No. 6011007th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York

```



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; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,365
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/400,256
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3985.220-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-975-365-39

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Query Match          51.5%; Score 302.5; DB 3; Length 137;
Best Local Similarity 50.0%; Pred. No. 4.6e-28;
Matches 70; Conservative 4; Mismatches 27; Indels 39; Gaps 4;

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Db      3 FPSI-----FTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVLPPFSN 57

QY      49 PLGTG-----PRFVNQHLCGSHLVEALYLVCGERGFFFYTPKTRG 87
      |
Db      58 STNNGLLFINTTIAASIAAKEEGVSMAKRFVNQHLCGSHLVEALYLVCGERGFFFYTPKTRG 117

QY      88 IVEQCCTSICSLYQLENYCN 107
      |||||
Db      118 IVEQCCTSICSLYQLENYCN 137

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RESULT 4

US-08-291-060B-5

; Sequence 5, Application US/08291060B
; Patent No. 5728543

GENERAL INFORMATION:

```

; APPLICANT: Dorschug, Michael
; APPLICANT: Koller, Klaus-Peter
; APPLICANT: Marquardt, Rudiger
; APPLICANT: Meiwes, Johannes
; TITLE OF INVENTION: An Enzymatic Process for the
; TITLE OF INVENTION: Conversion of Preproinsulins Into Insulins

```


; ADDRESSEE: Kenneth A. Genoni, Esq.
 ; STREET: Rt. 202-206 No. 5473049th/P.O. Box 2500
 ; CITY: Somerville
 ; STATE: New Jersey
 ; COUNTRY: U.S.A.
 ; ZIP: 08876-1258
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
 ; COMPUTER: IBM 386
 ; OPERATING SYSTEM: WINDOWS 3.1
 ; SOFTWARE: WORDPERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/160,376A
 ; FILING DATE: December 1, 1993
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GE P 4240420.7
 ; FILING DATE: December 2, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Barbara V. Maurer, Esq.
 ; REGISTRATION NUMBER: 31,287
 ; REFERENCE/DOCKET NUMBER: HOE 92/F 384
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (908) 231-4079
 ; TELEFAX: (908) 231-2255
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 56 Amino Acids
 ; TYPE: Amino Acid (AA)
 ; TOPOLOGY: not relevant
 US-08-160-376A-7

Query Match 50.9%; Score 299; DB 1; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3.9e-28;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
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 Db 4 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 56

RESULT 6
 US-08-389-487-11
 ; Sequence 11, Application US/08389487
 ; Patent No. 5663291
 ; GENERAL INFORMATION:
 ; APPLICANT: Obermeier, Rainer
 ; APPLICANT: Gerl, Martin
 ; APPLICANT: Ludwig, Jurgen
 ; APPLICANT: Sabel, Walter
 ; TITLE OF INVENTION: Process for Obtaining Insulin Having
 ; TITLE OF INVENTION: Correctly Linked Cystine Bridges
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESSEE: Dunner
 ; STREET: 1300 I Street, N.W.

```

;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: United States of America
;   ZIP: 20005-3315
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/389,487
;   FILING DATE:
;   CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Einaudi, Carol P.
;   REGISTRATION NUMBER: 32,220
;   REFERENCE/DOCKET NUMBER: 02481.1424-00000
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-408-4000
;   TELEFAX: 202-408-4400
;   INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 56 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-389-487-11

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Query Match          50.9%; Score 299; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 3.9e-28;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7

US-08-160-376A-5

; Sequence 5, Application US/08160376A

; Patent No. 5473049

; GENERAL INFORMATION:

; APPLICANT: Obermeier, Ranier

; APPLICANT: Gerl, Martin

; APPLICANT: Ludwig, Jurgen

; APPLICANT: Sabel, Walter

; TITLE OF INVENTION: Process For Obtaining Proinsulin

; TITLE OF INVENTION: Possessing Correctly Linked

; TITLE OF INVENTION: Cystine Bridges

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kenneth A. Genoni, Esq.

; STREET: Rt. 202-206 No. 5473049th/P.O. Box 2500

; CITY: Somerville

; STATE: New Jersey

; COUNTRY: U.S.A.

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; ZIP: 08876-1258
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 386
; OPERATING SYSTEM: WINDOWS 3.1
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/160,376A
; FILING DATE: December 1, 1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GE P 4240420.7
; FILING DATE: December 2, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barbara V. Maurer, Esq.
; REGISTRATION NUMBER: 31,287
; REFERENCE/DOCKET NUMBER: HOE 92/F 384
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 231-4079
; TELEFAX: (908) 231-2255
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 Amino Acids
; TYPE: Amino Acid (AA)
; TOPOLOGY: not relevant
US-08-160-376A-5

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```

Query Match          50.9%; Score 299; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 7.6e-28;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      55 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
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Db      44 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 96

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RESULT 8

US-08-389-487-8

; Sequence 8, Application US/08389487

; Patent No. 5663291

; GENERAL INFORMATION:

; APPLICANT: Obermeier, Rainer

; APPLICANT: Gerl, Martin

; APPLICANT: Ludwig, Jorgen

; APPLICANT: Sabel, Walter

; TITLE OF INVENTION: Process for Obtaining Insulin Having

; TITLE OF INVENTION: Correctly Linked Cystine Bridges

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: United States of America

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/389,487
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Einaudi, Carol P.
; REGISTRATION NUMBER: 32,220
; REFERENCE/DOCKET NUMBER: 02481.1424-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-389-487-8

```

```

Query Match          50.9%; Score 299; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 7.6e-28;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      55 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
        |||||
Db      44 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 96

```

RESULT 9

US-08-400-256-45

; Sequence 45, Application US/08400256

; Patent No. 5750497

; GENERAL INFORMATION:

; APPLICANT: Havelund, Svend

; APPLICANT: Halstrom, John

; APPLICANT: Jonassen, Ib

; APPLICANT: Andersen, Asser Sloth

; APPLICANT: Markussen, Jan

; TITLE OF INVENTION: ACYLATED INSULIN

; NUMBER OF SEQUENCES: 49

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 5750497o No. 5750497disk of No. 5750497th America, Inc.

; STREET: 405 Lexington Avenue, 64th Floor

; CITY: New York

; STATE: New York

; COUNTRY: United States of America

; ZIP: 10174-6401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/400,256
; FILING DATE: 03-MAR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3985.220-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-400-256-45

```

```

Query Match          50.9%; Score 299; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.3e-27;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      55 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      93 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 145

```

RESULT 10

```

US-08-975-365-45
; Sequence 45, Application US/08975365
; Patent No. 6011007
; GENERAL INFORMATION:
; APPLICANT: Havelund, Svend
; APPLICANT: Halstrom, John
; APPLICANT: Jonassen, Ib
; APPLICANT: Andersen, Asser Sloth
; APPLICANT: Markussen, Jan
; TITLE OF INVENTION: ACYLATED INSULIN
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6011007o No. 6011007disk of No. 6011007th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,365
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: US 08/400,256
 ; FILING DATE: 03-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lambiris, Elias J.
 ; REGISTRATION NUMBER: 33,728
 ; REFERENCE/DOCKET NUMBER: 3985.220-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-878-9655
 ; INFORMATION FOR SEQ ID NO: 45:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 145 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-975-365-45

Query Match 50.9%; Score 299; DB 3; Length 145;
 Best Local Similarity 100.0%; Pred. No. 1.3e-27;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
 |||
 Db 93 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 145

RESULT 11

US-08-400-256-48

; Sequence 48, Application US/08400256
 ; Patent No. 5750497
 ; GENERAL INFORMATION:
 ; APPLICANT: Havelund, Svend
 ; APPLICANT: Halstrom, John
 ; APPLICANT: Jonassen, Ib
 ; APPLICANT: Andersen, Asser Sloth
 ; APPLICANT: Markussen, Jan
 ; TITLE OF INVENTION: ACYLATED INSULIN
 ; NUMBER OF SEQUENCES: 49
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 5750497o No. 5750497disk of No. 5750497th America, Inc.
 ; STREET: 405 Lexington Avenue, 64th Floor
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States of America
 ; ZIP: 10174-6401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/400,256
 ; FILING DATE: 03-MAR-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lambiris, Elias J.
 ; REGISTRATION NUMBER: 33,728


```

; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-975-365-48

```

Query Match 50.9%; Score 299; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.3e-27;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

RESULT 13

US-08-030-731A-44

; Sequence 44, Application US/08030731A

; Patent No. 5426036

; GENERAL INFORMATION:

; APPLICANT: Koller, Klaus-Peter

; APPLICANT: Riess, Guenther Johannes

; APPLICANT: Uhlmann, Eugen

; APPLICANT: Wallmeier, Holger

10 TITLE OF INVENTION: Processes for the Preparation of Foreign

TITLE OF INVENTION: Proteins in Streptomyces

; NUMBER OF SEQUENCES: 48

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I Street, N.W., Suite 700

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

```
; MEDIUM TYPE: Floppy disk
```

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;      COMPUTER:  IBM PC compatible
```

```
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
```

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;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
```

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; CURRENT APPLICATION DATA:
```

; APPLICATION NUMBER: US/08/030,731A

; FILING DATE: 12-MAR-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/189,840

; FILING DATE: 03-MAY-1988

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/430,622

; FILING DATE: 01-NOV-1989

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/687,610

FILING DATE: 19-APR-1991

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,757
; FILING DATE: 29-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 37 14 866.4
; FILING DATE: 05-MAY-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 38 37 273.8
; FILING DATE: 03-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 39 27 449.7
; FILING DATE: 19-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 40 12 818.0
; FILING DATE: 21-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Kirschner Michael K.
; REGISTRATION NUMBER: 34,851
; REFERENCE/DOCKET NUMBER: 02481-0593-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 57 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-030-731A-44

```

```

Query Match          49.9%; Score 293; DB 1; Length 57;
Best Local Similarity 96.2%; Pred. No. 2.1e-27;
Matches 51; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      55 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
      :|||||
Db      5 KFVNQHLCGSHLVEALYLVCGERGFFYTPKTKGIVEQCCTSICSLYQLENYCN 57

```

RESULT 14

US-08-900-574-3

; Sequence 3, Application US/08900574

; Patent No. 6221837

; GENERAL INFORMATION:

; APPLICANT: Ertl, Johann

; APPLICANT: Habermann, Paul

; APPLICANT: Geisen, Karl

; APPLICANT: Seipke, Gerhard

; TITLE OF INVENTION: Insulin derivatives with increased zinc

; TITLE OF INVENTION: binding

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett,

; ADDRESSEE: & Dunner, L.L.P.

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: District of Columbia

```

; COUNTRY: U.S.A.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,574
; FILING DATE: July 24, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: German Application No. 6221837 19630242.0
; FILING DATE: July 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Carol P. Einaudi
; REGISTRATION NUMBER: 32,220
; REFERENCE/DOCKET NUMBER: 02481.1499-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 65 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..65
US-08-900-574-3

```

```

Query Match          48.9%; Score 287; DB 3; Length 65;
Best Local Similarity 91.4%; Pred. No. 1.2e-26;
Matches 53; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

```

```

Qy      51 GTGPRFVNQHLCGSHLVEALYLVCGERGFFYTPKT--RGIVEQCCTSICSLYQLENYC 106
      |  |||
Db      7  GNSARFVNQHLCGSHLVEALYLVCGERGFFYTPKTHHRGIVEQCCTSICSLYQLENYC 64

```

RESULT 15

US-08-900-574-5

```

; Sequence 5, Application US/08900574
; Patent No. 6221837
; GENERAL INFORMATION:
; APPLICANT: Ertl, Johann
; APPLICANT: Habermann, Paul
; APPLICANT: Geisen, Karl
; APPLICANT: Seipke, Gerhard
; TITLE OF INVENTION: Insulin derivatives with increased zinc
; TITLE OF INVENTION: binding
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:

```

```

;   ADDRESSEE: Finnegan, Henderson, Farabow, Garrett,
;   ADDRESSEE: & Dunner, L.L.P.
;   STREET: 1300 I Street, N.W.
;   CITY: Washington
;   STATE: District of Columbia
;   COUNTRY: U.S.A.
;   ZIP: 20005-3315
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/900,574
;   FILING DATE: July 24, 1997
;   CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: German Application No. 6221837 19630242.0
;   FILING DATE: July 26, 1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Carol P. Einaudi
;   REGISTRATION NUMBER: 32,220
;   REFERENCE/DOCKET NUMBER: 02481.1499-00000
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 408-4000
;   TELEFAX: (202) 408-4400
;   INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 66 amino acids
;   TYPE: Amino acid
;   STRANDEDNESS: Single
;   TOPOLOGY: linear
;   MOLECULE TYPE: Protein
;   ORIGINAL SOURCE:
;   ORGANISM: Escherichia coli
;   FEATURE:
;   NAME/KEY: Protein
;   LOCATION: 1..66
US-08-900-574-5

```

```

Query Match          48.8%; Score 286.5; DB 3; Length 66;
Best Local Similarity 89.8%; Pred. No. 1.4e-26;
Matches 53; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

```

```

Qy      51 GTGPRFVNQHLCGSHLVEALYLVCGERGFFYTPKT---RGIVEQCCTSICSLYQLENYC 106
      |  |||||||||||||||||||||||||||||  |||||||||||||||||||
Db      7  GNSARFVNQHLCGSHLVEALYLVCGERGFFYTPKTAHHRGIVEQCCTSICSLYQLENYC 65

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Search completed: February 11, 2005, 18:27:06
Job time : 28.2306 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 17:42:33 ; Search time 20.334 Seconds
(without alignments)
506.306 Million cell updates/sec

Title: US-10-054-873-6
Perfect score: 587
Sequence: 1 MFPTIPLSRFLFDNAMLRAHR.....IVEQCCTSICSLYQLENYCN 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	275	46.8	96	2 PC7082	epidermal growth f
2	273.5	46.6	51	1 INEL	insulin - elephant
3	273.5	46.6	51	1 INWHF	insulin - finback
4	273.5	46.6	51	1 INWHP	insulin - sperm wh
5	273	46.5	110	2 B42179	insulin precursor
6	273	46.5	110	2 JQ0178	insulin precursor
7	271.5	46.3	51	1 INHY	insulin - hamster
8	268.5	45.7	51	1 INMSSP	insulin - Egyptian
9	267.5	45.6	51	2 A59151	insulin precursor
10	267	45.5	110	1 IPHU	insulin precursor
11	267	45.5	110	2 A42179	insulin precursor
12	263.5	44.9	51	1 INCMA	insulin - Arabian
13	263.5	44.9	51	1 INGT	insulin - goat

14	263.5	44.9	51	1	INWH1S	insulin - sei whal
15	263	44.8	84	1	IPPG	insulin precursor
16	263	44.8	110	1	INRB	insulin precursor
17	262.5	44.7	51	1	INCT	insulin - cat
18	262	44.6	110	1	IPDG	insulin precursor
19	261.5	44.5	51	1	INMKSQ	insulin - common s
20	260	44.3	110	2	I48166	insulin precursor
21	258.5	44.0	105	1	IPBO	insulin precursor
22	257	43.8	108	2	A39883	insulin precursor
23	256.5	43.7	51	2	JQ0362	insulin - North Am
24	255.5	43.5	217	1	STHU	somatotropin 1 pre
25	255.5	43.5	217	2	I67410	somatotropin - rhe
26	252.5	43.0	77	1	INSH	insulin precursor
27	252	42.9	86	1	IPHO	insulin precursor
28	251.5	42.8	51	1	INCB	insulin - Chinchil
29	250	42.6	108	1	INMS1	insulin 1 precurs
30	249	42.4	110	1	IPRT1	insulin 1 precurs
31	248.5	42.3	51	1	INGS	insulin - goose
32	248	42.2	110	1	INMS2	insulin 2 precurs
33	248	42.2	110	1	IPRT2	insulin 2 precurs
34	246	41.9	52	2	S44470	insulin I2 - North
35	246	41.9	52	2	S44469	insulin I1 - North
36	245	41.7	103	2	I51221	insulin precursor
37	244.5	41.7	51	1	INOS	insulin - ostrich
38	244.5	41.7	51	1	INTK	insulin - turkey (
39	244.5	41.7	51	1	A61129	insulin - black-be
40	244.5	41.7	51	1	INPQ	insulin - crested
41	244.5	41.7	51	2	A60414	insulin - slider t
42	239.5	40.8	107	1	IPCH	insulin precursor
43	238	40.5	52	2	S61361	insulin - Amphiuma
44	235.5	40.1	51	2	S63590	insulin - duckbill
45	233.5	39.8	81	1	IPDK	insulin precursor

ALIGNMENTS

RESULT 1

PC7082

epidermal growth factor/single chain insulin fusion protein - *Bacillus brevis*
(fragment)

C;Species: *Bacillus brevis*

C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004

C;Accession: PC7082; PC7083

R;Koh, M.; Hanagata, H.; Ebisu, S.; Morihara, K.; Takagi, H.

Biosci. Biotechnol. Biochem. 64, 1079-1081, 2000

A;Title: Use of *Bacillus brevis* for synthesis and secretion of Des-B30 single-chain human insulin precursor.

A;Reference number: PC7082; MUID:20335834; PMID:10879487

A;Accession: PC7082

A;Molecule type: DNA

A;Residues: 1-96 <KOH>

A;Cross-references: UNIPROT:Q7MOU6

A;Accession: PC7083

A;Molecule type: protein

A;Residues: 19-28 <KO2>

C;Genetics:

A;Gene: egf-sci
C;Superfamily: insulin

Query Match 46.8%; Score 275; DB 2; Length 96;
Best Local Similarity 94.3%; Pred. No. 2.3e-21;
Matches 50; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

Qy 55 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
:||||| :
Db 46 KFVNQHLCGSHLVEALYLVCGERGFFYTPK--GIVEQCCTSICSLYQLENYCN 96

RESULT 2

INEL

insulin - elephant

C;Species: Elephantidae gen. sp. (elephant)

C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999

C;Accession: A01584

R;Smith, L.F.

Am. J. Med. 40, 662-666, 1966

A;Title: Species variation in the amino acid sequence of insulin.

A;Reference number: A90029; MUID:66160119; PMID:5949593

A;Accession: A01584

A;Molecule type: protein

A;Residues: 1-30;31-51 <SMI>

A;Note: the species of elephant is not given, but it is most probably the Indian elephant (*Elephas maximus*)

C;Superfamily: insulin

C;Keywords: hormone; pancreas

F;1-30/Domain: insulin chain B #status experimental <BCH>

F;1-30,31-51/Product: insulin #status experimental <MAT>

F;31-51/Domain: insulin chain A #status experimental <ACH>

F;7-37,19-50,36-41/Disulfide bonds: #status predicted

Query Match 46.6%; Score 273.5; DB 1; Length 51;
Best Local Similarity 94.2%; Pred. No. 1.7e-21;
Matches 49; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
||||| :
Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKT-GIVEQCCTGVCSLYQLENYCN 51

RESULT 3

INWHF

insulin - finback whale (tentative sequence)

C;Species: Balaenoptera physalus (finback whale, common rorqual)

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C;Accession: A91918

R;Hama, H.; Titani, K.; Sakaki, S.; Narita, K.

J. Biochem. 56, 285-293, 1964

A;Title: The amino acid sequence in fin-whale insulin.

A;Reference number: A91918

A;Accession: A91918

A;Molecule type: protein

A;Residues: 1-30;31-51 <HAM>

A;Cross-references: UNIPROT:P01312

C;Superfamily: insulin
 C;Keywords: hormone; pancreas
 F;1-30/Domain: insulin chain B #status experimental <BCH>
 F;1-30,31-51/Product: insulin #status experimental <MAT>
 F;31-51/Domain: insulin chain A #status experimental <ACH>
 F;7-37,19-50,36-41/Disulfide bonds: #status predicted

Query Match 46.6%; Score 273.5; DB 1; Length 51;
 Best Local Similarity 96.2%; Pred. No. 1.7e-21;
 Matches 50; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
 |||||
 Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKA-GIVEQCCTSICSLYQLENYCN 51

RESULT 4

INWHP

insulin - sperm whale

C;Species: Physeter catodon (sperm whale)

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C;Accession: A93142; A90082

R;Ishihara, Y.; Saito, T.; Ito, Y.; Fujino, M.

Nature 181, 1468-1469, 1958

A;Title: Structure of sperm- and sei-whale insulins and their breakdown by whale pepsin.

A;Reference number: A93142

A;Accession: A93142

A;Molecule type: protein

A;Residues: 1-30;31-51 <ISH>

A;Cross-references: UNIPROT:P01312

R;Harris, J.I.; Sanger, F.; Naughton, M.A.

Arch. Biochem. Biophys. 65, 427-428, 1956

A;Title: Species differences in insulin.

A;Reference number: A90082

A;Accession: A90082

A;Molecule type: protein

A;Residues: 1-30;31-51 <HAR>

C;Superfamily: insulin

C;Keywords: hormone; pancreas

F;1-30/Domain: insulin chain B #status experimental <BCH>

F;1-30,31-51/Product: insulin #status experimental <MAT>

F;31-51/Domain: insulin chain A #status experimental <ACH>

F;7-37,19-50,36-41/Disulfide bonds: #status predicted

Query Match 46.6%; Score 273.5; DB 1; Length 51;
 Best Local Similarity 96.2%; Pred. No. 1.7e-21;
 Matches 50; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
 |||||
 Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKA-GIVEQCCTSICSLYQLENYCN 51

RESULT 5

B42179

insulin precursor - green monkey

A;Accession: JQ0178
 A;Molecule type: mRNA
 A;Residues: 1-110 <WET>
 A;Cross-references: UNIPROT:P30406; GB:J00336; NID:g342121; PIDN:AAA36849.1;
 PID:g342122
 C;Superfamily: insulin
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-54,90-110/Product: insulin #status predicted <MAT>
 F;25-54/Domain: insulin chain B #status predicted <BCH>
 F;55-89/Domain: insulin connecting C peptide #status predicted <CPT>
 F;90-110/Domain: insulin chain A #status predicted <ACH>
 F;31-96,43-109,95-100/Disulfide bonds: #status predicted

Query Match 46.5%; Score 273; DB 2; Length 110;
 Best Local Similarity 60.2%; Pred. No. 4.2e-21;
 Matches 53; Conservative 0; Mismatches 1; Indels 34; Gaps 1;

```
Qy      54 PRFVNQHLCGSHLVEALYLVCGERGFFYTPKT----- 85
          | |||||
Db      23 PAFVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDPQVGQVELGGGPGAGSLQPLAL 82

Qy      86 -----RGIVEQCCTSICSLYQLENYCN 107
          |||||
Db      83 EGS LQKRGIVEQCCTSICSLYQLENYCN 110
```

RESULT 7

INHY

insulin - hamster

C;Species: Cricetinae gen. sp. (hamster)

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999

C;Accession: A91456

R;Neelon, F.A.; Delcher, H.K.; Steinman, H.; Lebovitz, H.E.

Fed. Proc. 32, 300, 1973

A;Title: Structure of hamster insulin: comparison with a tumor insulin.

A;Reference number: A91456

A;Accession: A91456

A;Molecule type: protein

A;Residues: 1-30;31-51 <NEE>

A;Cross-references: UNIPROT:Q7MOG1

C;Superfamily: insulin

C;Keywords: hormone; pancreas

F;1-30/Domain: insulin chain B #status experimental <BCH>

F;1-30,31-51/Product: insulin #status experimental <MAT>

F;31-51/Domain: insulin chain A #status experimental <ACH>

F;7-37,19-50,36-41/Disulfide bonds: #status predicted

Query Match 46.3%; Score 271.5; DB 1; Length 51;
 Best Local Similarity 94.2%; Pred. No. 2.7e-21;
 Matches 49; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

```
Qy      56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
          |||||:|||||
Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKS-GIVDQCCTSICSLYQLENYCN 51
```

RESULT 8

INMSSP

insulin - Egyptian spiny mouse (tentative sequence)
C;Species: *Acomys cahirinus* (Egyptian spiny mouse)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004
C;Accession: A01591
R;Buenzli, H.F.; Humbel, R.E.
Hoppe-Seyler's Z. Physiol. Chem. 353, 444-450, 1972
A;Title: Isolation and partial structural analysis of insulin from mouse (*Mus musculus*) and spiny mouse (*Acomys cahirinus*).
A;Reference number: A01591; MUID:72189454; PMID:5028210
A;Contents: composition
A;Accession: A01591
A;Molecule type: protein
A;Residues: 1-30;31-51 <BUE>
A;Cross-references: UNIPROT:P01324
C;Superfamily: insulin
C;Keywords: hormone; pancreas
F;1-30/Domain: insulin chain B #status predicted <BCH>
F;1-30,31-51/Product: insulin #status predicted <MAT>
F;31-51/Domain: insulin chain A #status predicted <ACH>
F;7-37,19-50,36-41/Disulfide bonds: #status predicted

Query Match 45.7%; Score 268.5; DB 1; Length 51;
Best Local Similarity 92.3%; Pred. No. 5.5e-21;
Matches 48; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy 56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
||:|||||||||||||||||||||||: ||:|||||||||||||||
Db 1 FVBQHLGSHLVEALYLVCGERGFFYTPKS-GIVDQCCTSICSLYQLENYCN 51

RESULT 9

A59151

insulin precursor - jack bean (fragments)

N;Alternate names: hypoglycemic agent; plant insulin

C;Species: *Canavalia ensiformis* (jack bean)

C;Date: 07-Dec-1999 #sequence_revision 07-Dec-1999 #text_change 10-Dec-1999

C;Accession: B59151; A59151

R;Oliveira, A.E.A.; Machado, O.L.T.; Gomes, V.M.; Xavier-Neto, J.; Pereira,

A.C.P.; Vieira, J.G.H.; Fernandes, K.V.S.; Xavier-Filho, J.

Protein Pept. Lett. 6, 15-21, 1999

A;Title: Jack bean seed coat contains a protein with complete sequence homology to bovine insulin.

A;Reference number: A59151

A;Accession: B59151

A;Molecule type: protein

A;Residues: 1-30 <MACB>

A;Cross-references: UNIPROT:Q7M217

A;Accession: A59151

A;Molecule type: protein

A;Residues: 31-51 <MACA>

C;Comment: The two chains are probably produced from the same precursor.

C;Superfamily: insulin

F;1-30,31-51/Product: insulin #status experimental <MAT>

F;1-30/Domain: chain B #status experimental <CHB>

F;31-51/Domain: chain A #status experimental <CHA>

F;7-37,19-50,36-41/Disulfide bonds: #status predicted

Query Match 45.6%; Score 267.5; DB 2; Length 51;
Best Local Similarity 92.3%; Pred. No. 7e-21;
Matches 48; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
||||| :|||||
Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKA-GIVEQCCASVCSLYQLENYCN 51

RESULT 10

IPHU

insulin precursor [validated] - human

N;Alternate names: preproinsulin

C;Species: Homo sapiens (man)

C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004

C;Accession: A93222; A94253; A93216; A94251; A93144; A92075; A91186; I58114; A01579; S58661

R;Bell, G.I.; Pictet, R.L.; Rutter, W.J.; Cordell, B.; Tischer, E.; Goodman, H.M.

Nature 284, 26-32, 1980

A;Title: Sequence of the human insulin gene.

A;Reference number: A93222; MUID:80120725; PMID:6243748

A;Accession: A93222

A;Molecule type: DNA

A;Residues: 1-110 <BEL>

A;Cross-references: UNIPROT:P01308; GB:J00265; NID:g186429; PIDN:AAA59172.1; PID:g386828

R;Ullrich, A.; Dull, T.J.; Gray, A.; Brosius, J.; Sures, I.

Science 209, 612-615, 1980

A;Title: Genetic variation in the human insulin gene.

A;Reference number: A94253; MUID:80236313; PMID:6248962

A;Accession: A94253

A;Molecule type: DNA

A;Residues: 1-110 <ULL>

A;Cross-references: GB:J00265; NID:g186429; PIDN:AAA59172.1; PID:g386828

R;Bell, G.I.; Swain, W.F.; Pictet, R.; Cordell, B.; Goodman, H.M.; Rutter, W.J.

Nature 282, 525-527, 1979

A;Title: Nucleotide sequence of a cDNA clone encoding human preproinsulin.

A;Reference number: A93216; MUID:80054779; PMID:503234

A;Accession: A93216

A;Molecule type: mRNA

A;Residues: 1-110 <BEL2>

A;Cross-references: GB:J00265; NID:g186429; PIDN:AAA59172.1; PID:g386828

R;Sures, I.; Goeddel, D.V.; Gray, A.; Ullrich, A.

Science 208, 57-59, 1980

A;Title: Nucleotide sequence of human preproinsulin complementary DNA.

A;Reference number: A94251; MUID:80147417; PMID:6927840

A;Accession: A94251

A;Molecule type: mRNA

A;Residues: 1-110 <SUR>

A;Cross-references: GB:J00265; NID:g186429; PIDN:AAA59172.1; PID:g386828

R;Nicol, D.S.H.W.; Smith, L.F.

Nature 187, 483-485, 1960

A;Title: Amino-acid sequence of human insulin.

A;Reference number: A93144

A;Accession: A93144

A;Molecule type: protein
 A;Residues: 25-54;90-110 <NIC>
 R;Oyer, P.E.; Cho, S.; Peterson, J.D.; Steiner, D.F.
 J. Biol. Chem. 246, 1375-1386, 1971
 A;Title: Studies on human proinsulin. Isolation and amino acid sequence of the human pancreatic C-peptide.
 A;Reference number: A92075; MUID:71116410; PMID:5101771
 A;Accession: A92075
 A;Molecule type: protein
 A;Residues: 57-87 <OYE>
 R;Ko, A.; Smyth, D.G.; Markussen, J.; Sundby, F.
 Eur. J. Biochem. 20, 190-199, 1971
 A;Title: Amino acid sequence of the C-peptide of human proinsulin.
 A;Reference number: A91186; MUID:71257722; PMID:5560404
 A;Accession: A91186
 A;Molecule type: protein
 A;Residues: 57-87 <KOA>
 R;Lucassen, A.M.; Julier, C.; Beressi, J.P.; Boitard, C.; Froguel, P.; Lathrop, M.; Bell, J.I.
 Nature Genet. 4, 305-310, 1993
 A;Title: Susceptibility to insulin dependent diabetes mellitus maps to a 4.1 kb segment of DNA spanning the insulin gene and associated VNTR.
 A;Reference number: I58114; MUID:93364428; PMID:8358440
 A;Accession: I58114
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-59,63-110 <RES>
 A;Cross-references: GB:L15440; NID:g307071; PIDN:AAA59179.1; PID:g307072
 R;Sieber, P.; Kamber, B.; Hartmann, A.; Joehl, A.; Riniker, B.; Rittel, W.
 Helv. Chim. Acta 57, 2617-2621, 1974
 A;Title: Totalsynthese von Humaninsulin unter gezielter Bildung der Disulfidbindungen.
 A;Reference number: A91636; MUID:75077277; PMID:4443293
 A;Contents: annotation; synthesis
 A;Note: disulfide-bonded human insulin was synthesized; the synthetic hormone was identical with the natural hormone in chemical and biological activities
 A;Note: article in German with English abstract
 R;Naithani, V.K.
 Hoppe-Seyler's Z. Physiol. Chem. 354, 659-672, 1973
 A;Title: The synthesis of C-peptide of human proinsulin.
 A;Reference number: A91658; MUID:75040007; PMID:4803504
 A;Contents: annotation; synthesis of residues 57-87
 R;Geiger, R.; Jaeger, G.; Koenig, W.
 Chem. Ber. 106, 2347-2352, 1973
 A;Title: Synthesis of the complete sequence of human proinsulin C-peptide and its [Glu-9,Gln-11] analogue.
 A;Reference number: A90914
 A;Contents: annotation; synthesis of residues 57-87
 R;Kaufmann, J.E.; Irminger, J.C.; Halban, P.A.
 Biochem. J. 310, 869-874, 1995
 A;Title: Sequence requirements for proinsulin processing at the B-chain/C-peptide junction.
 A;Reference number: S58661; MUID:96013185; PMID:7575420
 A;Contents: annotation; site-directed mutagenesis study of proteolytic processing
 C;Genetics:
 A;Gene: GDB:INS

A;Cross-references: GDB:119349; OMIM:176730
A;Map position: 11p15.5-11p15.5
A;Introns: 63/1
C;Superfamily: insulin
C;Keywords: hormone; pancreas
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-54/Domain: insulin chain B #status experimental <BCH>
F;25-54,90-110/Product: insulin #status experimental <MAT>
F;57-87/Domain: connecting C peptide #status experimental <CPEP>
F;90-110/Domain: insulin chain A #status experimental <ACH>
F;31-96,43-109,95-100/Disulfide bonds: #status experimental

Query Match 45.5%; Score 267; DB 1; Length 110;
Best Local Similarity 60.5%; Pred. No. 1.8e-20;
Matches 52; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

```
QY      56 FVNQHLCGSHLVEALYLVCGERGFFYTPKT----- 85
      ||||||||||||||||||||||||||||
Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84

QY      86 ----RGIVEQCCTSICSLYQLENYCN 107
      |||||||||||||||||||
Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110
```

RESULT 11

A42179

insulin precursor - chimpanzee

C;Species: Pan troglodytes (chimpanzee)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A42179; S22058

R;Seino, S.; Bell, G.I.; Li, W.H.

Mol. Biol. Evol. 9, 193-203, 1992

A;Title: Sequences of primate insulin genes support the hypothesis of a slower rate of molecular evolution in humans and apes than in monkeys.

A;Reference number: A42179; MUID:92219953; PMID:1560757

A;Accession: A42179

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-110 <SEI>

A;Cross-references: UNIPROT:P30410; EMBL:X61089; NID:g38251; PIDN:CAA43403.1; PID:g38252

A;Note: sequence extracted from NCBI backbone (NCBIP:95067)

C;Genetics:

A;Introns: 63/1

C;Superfamily: insulin

Query Match 45.5%; Score 267; DB 2; Length 110;
Best Local Similarity 60.5%; Pred. No. 1.8e-20;
Matches 52; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

```
QY      56 FVNQHLCGSHLVEALYLVCGERGFFYTPKT----- 85
      ||||||||||||||||||||||||||||
Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84

QY      86 ----RGIVEQCCTSICSLYQLENYCN 107
      |||||||||||||||||||
```

Db

RESULT 12

INCMA

insulin - Arabian camel (tentative sequence)

C;Species: Camelus dromedarius (Arabian camel)

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C;Accession: A92782

R; Danho, W.O.

J. Fac. Med. Baghdad 14, 16-28, 1972

A:Title: The isolation and characterization of insulin of camel (Camelus dromedarius).

A;Reference number: A92782

A;Accession: A92782

A;Molecule type: protein

A;Residues: 1-30;31-51 <DAN>

A;Cross-references: UNIPROT:P01320

C;Superfamily: insulin

C; Keywords: hormone; pancreas

F;1-30/Domain: insulin chain B #status experimental <BCH>

F;1-30,31-51/Product: insulin #status experimental <MAT>

F;31-51/Domain: insulin chain A #status experimental <ACH>

F;7-37,19-50,36-41/Disulfide bonds: #status predicted

Query Match 44.9%; Score 263.5; DB 1; Length 51;
Best Local Similarity 90.4%; Pred. No. 1.8e-20;
Matches 47; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSIICSLYQLENYCN 107
| | | | | | | | | | | | | | | | | | | | | : | | | | | | |
Db 1 FANQHLCGSHLVEALYLVCGERGFFYTPKA-GIVEQCCASVCSLYQLENYCN 51

RESULT 13

INGT

insulin - goat

C;Species: Capra aegagrus hircus (domestic goat)

C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004

C;Accession: A01586

R;Smith, L.F.

Am. J. Med. 40, 662-666, 1966

A;Title: Species variation in the amino acid sequence of insulin.

A;Reference number: A90029; MUID:66160119; PMID:5949593

A;Accession: A01586

A;Molecule type: protein

A;Residues: 1-30;31-51 <SMI>

A;Cross-references: UNIPROT:P01319

C;Superfamily: insulin

C;Keywords: hormone; pancreas

F;1-30/Domain: insulin chain B #status experimental <BCH>

F;1-30,31-51/Product: insulin #status experimental <MAT>

F;31-51/Domain: insulin chain A #status experimental <ACH>

F;7-37,19-50,36-41/Disulfide bonds: #status predicted

Query Match 44.9%; Score 263.5; DB 1; Length 51;
Best Local Similarity 90.4%; Pred. No. 1.8e-20;

Matches 47; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

```
Qy      56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSSLYQLENYCN 107
          |||||
Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKA-GIVEQCCAGVCSLYQLENYCN 51
```

RESULT 14

INWH1S

insulin - sei whale

C;Species: Balaenoptera borealis (sei whale)

C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004

C;Accession: A01582

R;Ishihara, Y.; Saito, T.; Ito, Y.; Fujino, M.

Nature 181, 1468-1469, 1958

A;Title: Structure of sperm- and sei-whale insulins and their breakdown by whale pepsin.

A;Reference number: A93142

A;Accession: A01582

A;Molecule type: protein

A;Residues: 1-30;31-51 <ISH>

A;Cross-references: UNIPROT:P01314

C;Superfamily: insulin

C;Keywords: hormone; pancreas

F;1-30/Domain: insulin chain B #status experimental <BCH>

F;1-30,31-51/Product: insulin #status experimental <MAT>

F;31-51/Domain: insulin chain A #status experimental <ACH>

F;7-37,19-50,36-41/Disulfide bonds: #status predicted

Query Match 44.9%; Score 263.5; DB 1; Length 51;

Best Local Similarity 92.3%; Pred. No. 1.8e-20;

Matches 48; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

```
Qy      56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSSLYQLENYCN 107
          |||||
Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKA-GIVEQCCASTCSLYQLENYCN 51
```

RESULT 15

IPPG

insulin precursor - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 22-Jun-1981 #sequence_revision 22-Jun-1981 #text_change 16-Jul-1999

C;Accession: A01583; A94572; S16492; A60835; B60835

R;Chance, R.E.; Ellis, R.M.; Bromer, W.W.

Science 161, 165-167, 1968

A;Title: Porcine proinsulin: characterization and amino acid sequence.

A;Reference number: A94240; MUID:68286485; PMID:5657063

A;Accession: A01583

A;Molecule type: protein

A;Residues: 1-34,'Q',36-84 <CHA>

R;Chance, R.E.

submitted to the Atlas, July 1970

A;Reference number: A94572

A;Accession: A94572

A;Molecule type: protein

A;Residues: 1-84 <CH2>

R;Brown, H.; Sanger, F.; Kitai, R.
 Biochem. J. 60, 556-565, 1955
 A;Title: The structure of pig and sheep insulins.
 A;Reference number: A90344
 A;Accession: S16492
 A;Molecule type: protein
 A;Residues: 1-30;31-51 <BRO>
 R;Snel, L.; Damgaard, U.
 Horm. Metab. Res. 20, 476-480, 1988
 A;Title: Proinsulin heterogeneity in pigs.
 A;Reference number: A60835; MUID:89032178; PMID:3181865
 A;Accession: A60835
 A;Molecule type: protein
 A;Residues: 33-38,40-62 <SNE>
 A;Note: the authors report the characterization of a connecting peptide variant lacking Ala-39
 A;Accession: B60835
 A;Molecule type: protein
 A;Residues: 33-62 <SN2>
 R;Blundell, T.; Dodson, G.; Hodgkin, D.; Mercola, D.
 Adv. Protein Chem. 26, 279-402, 1972
 A;Title: Insulin. the structure in the crystal and its reflection in chemistry and biology.
 A;Reference number: A90017
 A;Contents: annotation; X-ray crystallography, 1.9 angstroms
 C;Superfamily: insulin
 C;Keywords: hormone; pancreas
 F;1-30/Domain: insulin chain B #status experimental <BCH>
 F;1-30,64-84/Product: insulin #status experimental <MAT>
 F;33-63/Domain: connecting peptide #status experimental <CPEP>
 F;64-84/Domain: insulin chain A #status experimental <ACH>
 F;7-70,19-83,69-74/Disulfide bonds: #status experimental

Query Match 44.8%; Score 263; DB 1; Length 84;
 Best Local Similarity 60.7%; Pred. No. 3.4e-20;
 Matches 51; Conservative 0; Mismatches 1; Indels 32; Gaps 1;

```

Qy      56 FVNQHLCGSHLVEALYLVCGERGFFYTPKT----- 85
          |||
Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKARREAENPQAGAVELGGGLGGLQALALEGPP 60

Qy      86 --RGIVEQCCTSICSLYQLENYCN 107
          |||
Db      61 QKRGIVEQCCTSICSLYQLENYCN 84

```

Search completed: February 11, 2005, 18:24:36
 Job time : 21.334 secs

OM protein - protein search, using sw model

Run on: February 11, 2005, 18:23:02 ; Search time 77.7823 Seconds
(without alignments)
449.487 Million cell updates/sec

Title: US-10-054-873-6
Perfect score: 587
Sequence: 1 MFPTIPLSRLFDNAMLRAHR.....IVEQCCTSICSILYQLENYCN 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	587	100.0	107	13	US-10-054-873-6	Sequence 6, Appli
2	555.5	94.6	150	13	US-10-054-873-7	Sequence 7, Appli
3	302.5	51.5	137	16	US-10-101-454-39	Sequence 39, Appl
4	299	50.9	145	16	US-10-101-454-45	Sequence 45, Appl
5	299	50.9	146	16	US-10-101-454-48	Sequence 48, Appl
6	294	50.1	52	13	US-10-054-873-5	Sequence 5, Appli
7	284.5	48.5	124	9	US-09-894-711-18	Sequence 18, Appl
8	284	48.4	138	9	US-09-861-687-19	Sequence 19, Appl
9	284	48.4	138	15	US-10-620-651-19	Sequence 19, Appl
10	284	48.4	140	16	US-10-101-454-33	Sequence 33, Appl
11	284	48.4	140	16	US-10-101-454-42	Sequence 42, Appl
12	281	47.9	104	16	US-10-101-454-15	Sequence 15, Appl
13	278.5	47.4	51	10	US-09-858-935B-5	Sequence 5, Appli
14	278.5	47.4	51	13	US-10-028-410-3	Sequence 3, Appli
15	278.5	47.4	51	14	US-10-444-326-3	Sequence 3, Appli
16	278.5	47.4	51	15	US-10-271-869-5	Sequence 5, Appli
17	278.5	47.4	51	15	US-10-444-262-3	Sequence 3, Appli
18	278.5	47.4	51	15	US-10-444-649-3	Sequence 3, Appli
19	278.5	47.4	51	15	US-10-444-701-3	Sequence 3, Appli
20	278	47.4	117	9	US-09-280-030-63	Sequence 63, Appl
21	277.5	47.3	124	15	US-10-221-677-24	Sequence 24, Appl
22	277	47.2	96	9	US-09-947-563-4	Sequence 4, Appli
23	277	47.2	102	16	US-10-101-454-36	Sequence 36, Appl
24	275.5	46.9	124	9	US-09-736-611-12	Sequence 12, Appl
25	275.5	46.9	124	9	US-09-740-359-12	Sequence 12, Appl
26	275.5	46.9	124	9	US-09-894-711-12	Sequence 12, Appl
27	275.5	46.9	124	14	US-10-316-421-12	Sequence 12, Appl
28	275.5	46.9	125	9	US-09-736-611-10	Sequence 10, Appl
29	275.5	46.9	125	9	US-09-740-359-10	Sequence 10, Appl
30	275.5	46.9	125	9	US-09-894-711-10	Sequence 10, Appl
31	275.5	46.9	125	14	US-10-316-421-10	Sequence 10, Appl
32	275.5	46.9	147	9	US-09-736-611-8	Sequence 8, Appli
33	275.5	46.9	147	9	US-09-740-359-7	Sequence 7, Appli
34	275.5	46.9	147	14	US-10-316-421-8	Sequence 8, Appli
35	274	46.7	144	9	US-09-736-611-6	Sequence 6, Appli
36	274	46.7	144	9	US-09-740-359-5	Sequence 5, Appli
37	274	46.7	144	14	US-10-316-421-6	Sequence 6, Appli
38	274	46.7	146	9	US-09-894-711-5	Sequence 5, Appli
39	273	46.5	50	13	US-10-066-009A-3	Sequence 3, Appli
40	271	46.2	96	9	US-09-947-563-5	Sequence 5, Appli
41	270	46.0	104	16	US-10-101-454-21	Sequence 21, Appl
42	270	46.0	104	16	US-10-101-454-27	Sequence 27, Appl
43	269.5	45.9	130	9	US-09-280-030-62	Sequence 62, Appl
44	269	45.8	104	16	US-10-101-454-24	Sequence 24, Appl
45	269	45.8	104	16	US-10-101-454-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1

US-10-054-873-6

; Sequence 6, Application US/10054873

; Publication No. US20020164712A1

```

; GENERAL INFORMATION:
; APPLICANT: Gan, Zhong Ru
; TITLE OF INVENTION: Chimeric Protein Containing an
;                      Intramolecular Chaperone-Like Sequence
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,873
; FILING DATE: 22-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/CN98/00052
; FILING DATE: 31-MAR-1998
; APPLICATION NUMBER: US 09/423,100
; FILING DATE: 11-DEC-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Mycroft, Frank J
; REGISTRATION NUMBER: 46,946
; REFERENCE/DOCKET NUMBER: 020167-000130US
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-054-873-6

```

```

Query Match          100.0%;  Score 587;  DB 13;  Length 107;
Best Local Similarity 100.0%;  Pred. No. 6.5e-61;
Matches 107;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

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Qy      1 MFPTIPLSRLFDNAMLRAHRLHQLAFDITYQEFEEAYIPKEQKYSFLQNPLGTGPREVNQH 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MFPTIPLSRLFDNAMLRAHRLHQLAFDITYQEFEEAYIPKEQKYSFLQNPLGTGPREVNQH 60

Qy     61 LCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107

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RESULT 2
US-10-054-873-7
; Sequence 7, Application US/10054873
; Publication No. US20020164712A1

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; GENERAL INFORMATION:
; APPLICANT: Gan, Zhong Ru
; TITLE OF INVENTION: Chimeric Protein Containing an
;                      Intramolecular Chaperone-Like Sequence
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,873
; FILING DATE: 22-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/CN98/00052
; FILING DATE: 31-MAR-1998
; APPLICATION NUMBER: US 09/423,100
; FILING DATE: 11-DEC-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Mycroft, Frank J
; REGISTRATION NUMBER: 46,946
; REFERENCE/DOCKET NUMBER: 020167-000130US
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-054-873-7

```

```

Query Match          94.6%; Score 555.5; DB 13; Length 150;
Best Local Similarity 71.3%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

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```

Qy      1 MFPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNP----- 49
        ||||||||||||||||||||||||||||||||||||||||||||
Db      1 MFPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSSESIP 60

Qy     50 -----LGTGPRFVNQHLCGSHLVEALYLVCGER 77
        ||||||||||||||||||||||||||||||||||||||||
Db     61 TPSNREETQQKSNLELLRISLLLIQSWLEPVQLGTGPRFVNQHLCGSHLVEALYLVCGER 120

Qy     78 GFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
        ||||||||||||||||||||||||||||
Db    121 GFFYTPKTRGIVEQCCTSICSLYQLENYCN 150

```


Db 58 STNNGLLFINTTIIASIAAKEEGVSMKRFBVNQHLGSHLVEALYLVCGERGFFYTPKTRG 117

Qy 88 IVEQCCTSICSLYQLENYCN 107
 |||

Db 118 IVEQCCTSICSLYQLENYCN 137

RESULT 4

US-10-101-454-45

; Sequence 45, Application US/10101454

; Publication No. US20040110664A1

; GENERAL INFORMATION:

; APPLICANT: Havelund, Svend
 ; Halstrom, John
 ; Jonassen, Ib
 ; Andersen, Asser Sloth
 ; Markussen, Jan

; TITLE OF INVENTION: ACYLATED INSULIN

; NUMBER OF SEQUENCES: 49

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Novo Nordisk of North America, Inc.
 ; STREET: 405 Lexington Avenue, 64th Floor
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States of America
 ; ZIP: 10174-6401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/101,454
 ; FILING DATE: 20-Mar-2002
 ; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/400,256
 ; FILING DATE: 03-MAR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Lambiris, Elias J.
 ; REGISTRATION NUMBER: 33,728
 ; REFERENCE/DOCKET NUMBER: 3985.220-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-878-9655

; INFORMATION FOR SEQ ID NO: 45:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 145 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 45:

US-10-101-454-45

Query Match 50.9%; Score 299; DB 16; Length 145;

Best Local Similarity 100.0%; Pred. No. 6.1e-27;

Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 93 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 145

RESULT 5

US-10-101-454-48

; Sequence 48, Application US/10101454

; Publication No. US20040110664A1

; GENERAL INFORMATION:

; APPLICANT: Havelund, Svend

; Halstrom, John

; Jonassen, Ib

; Andersen, Asser Sloth

; Markussen, Jan

; TITLE OF INVENTION: ACYLATED INSULIN

; NUMBER OF SEQUENCES: 49

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Novo Nordisk of North America, Inc.

; STREET: 405 Lexington Avenue, 64th Floor

; CITY: New York

; STATE: New York

; COUNTRY: United States of America

; ZIP: 10174-6401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/101,454

; FILING DATE: 20-Mar-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/400,256

; FILING DATE: 03-MAR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Lambiris, Elias J.

; REGISTRATION NUMBER: 33,728

; REFERENCE/DOCKET NUMBER: 3985.220-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-867-0123

; TELEFAX: 212-878-9655

; INFORMATION FOR SEQ ID NO: 48:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 146 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 48:

US-10-101-454-48

Query Match 50.9%; Score 299; DB 16; Length 146;

Best Local Similarity 100.0%; Pred. No. 6.2e-27;

Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
 ||||||||||||||||||
 Db 94 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 146

RESULT 6

US-10-054-873-5

; Sequence 5, Application US/10054873

; Publication No. US20020164712A1

; GENERAL INFORMATION:

; APPLICANT: Gan, Zhong Ru

; TITLE OF INVENTION: Chimeric Protein Containing an
 ; Intramolecular Chaperone-Like Sequence

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/054,873

; FILING DATE: 22-Jan-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/CN98/00052

; FILING DATE: 31-MAR-1998

; APPLICATION NUMBER: US 09/423,100

; FILING DATE: 11-DEC-2000

; ATTORNEY/AGENT INFORMATION:

; NAME: Mycroft, Frank J

; REGISTRATION NUMBER: 46,946

; REFERENCE/DOCKET NUMBER: 020167-000130US

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 52 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-054-873-5

Query Match 50.1%; Score 294; DB 13; Length 52;

Best Local Similarity 100.0%; Pred. No. 6.8e-27;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
 ||||||||||||||||||

Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 52

RESULT 7

US-09-894-711-18

; Sequence 18, Application US/09894711
; Patent No. US20020137144A1
; GENERAL INFORMATION:
; APPLICANT: Kjeldsen, Thomas Borglum
; APPLICANT: Ludvigsen, Svend
; TITLE OF INVENTION: Method for making insulin precursors and
; TITLE OF INVENTION: insulin precursor analogues having improved fermentation
; TITLE OF INVENTION: yield in yeast
; FILE REFERENCE: 6148.400-US
; CURRENT APPLICATION NUMBER: US/09/894,711
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PA 2000 00443
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: PA 1999 01869
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 60/211,081
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 60/181,450
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 09/740,359
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-894-711-18

Query Match 48.5%; Score 284.5; DB 9; Length 124;
Best Local Similarity 92.7%; Pred. No. 2.6e-25;
Matches 51; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 54 PRFVNQHLCGSHLVEALYLVCGERGFFYTPK-TRGIVEQCCTSICSLYQLENYCN 107
|:|||||||||||||||||||||:|||||||||||||||||
Db 70 PKFVNQHLCGSHLVEALYLVCGERGFFYTPKAAKGIVEQCCTSICSLYQLENYCN 124

RESULT 8

US-09-861-687-19

; Sequence 19, Application US/09861687
; Publication No. US20020193292A1
; GENERAL INFORMATION:
; APPLICANT: Markussen, Jan
; Jonassen, Ib
; Havelund, Svend
; Brandt, Jakob
; Kurtzhals, Peter
; Hansen, Hertz Per
; Kaarsholm, Niels Christian
; TITLE OF INVENTION: INSULIN DERIVATIVES
; NUMBER OF SEQUENCES: 26

```

;      CORRESPONDENCE ADDRESS:
;      ADDRESSEE: No. US20020193292A1o No. US20020193292Aldisk of No.
US20020193292A1th America, Inc.
;      STREET: 405 Lexington Avenue, 64th Floor
;      CITY: New York
;      STATE: New York
;      COUNTRY: United States of America
;      ZIP: 10174-6401
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/861,687
;      FILING DATE: 21-May-2001
;      CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/932,082
;      FILING DATE: 16-DEC-1997
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Lambiris, Elias J.
;      REGISTRATION NUMBER: 33,728
;      REFERENCE/DOCKET NUMBER: 4341.204-US
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 212-867-0123
;      TELEFAX: 212-878-9655
;      INFORMATION FOR SEQ ID NO: 19:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 138 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-861-687-19

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Query Match          48.4%; Score 284; DB 9; Length 138;
Best Local Similarity 48.2%; Pred. No. 3.3e-25;
Matches 68; Conservative 5; Mismatches 28; Indels 40; Gaps 5;

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Qy      2  FPTIPLSR LFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQ--KYSFLQ-----N 48
      ||:|      |      :      |      :|      ||      ||      ||      |
Db      3  FPSI-----FTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVL PFSN 57

Qy      49  PLGTG-----PRFVNQHLCGSHLVEALYLVCGERGFFYTPK-TR 86
      |      |||||||||||||||||||||||||||||      :
Db      58  STNNGLLFINTTIIASIAAKEEGVSLDKRFVNQHLCGSHLVEALYLVCGERGFFYTPKAAK 117

Qy      87  GIVEQCCTSICSLYQLENYCN 107
      |||||||||||||||||||
Db      118 GIVEQCCTSICSLYQLENYCN 138

```

```

RESULT 9
US-10-620-651-19
; Sequence 19, Application US/10620651
; Publication No. US20040067874A1

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Qy 87 GIVEQCCTSICSLYQLENYCN 107
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Db 118 GIVEQCCTSICSLYQLENYCN 138

RESULT 10

US-10-101-454-33

; Sequence 33, Application US/10101454

; Publication No. US20040110664A1

; GENERAL INFORMATION:

; APPLICANT: Havelund, Svend
; Halstrom, John
; Jonassen, Ib
; Andersen, Asser Sloth
; Markussen, Jan

; TITLE OF INVENTION: ACYLATED INSULIN

; NUMBER OF SEQUENCES: 49

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/101,454
; FILING DATE: 20-Mar-2002
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/400,256
; FILING DATE: 03-MAR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3985.220-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 33:

US-10-101-454-33

Query Match 48.4%; Score 284; DB 16; Length 140;
Best Local Similarity 47.6%; Pred. No. 3.4e-25;
Matches 68; Conservative 6; Mismatches 27; Indels 42; Gaps 5;

Qy 2 FPTIPLSRLFDNAMLRAHRLHQLAFD TYQEFEEAYIPKEQ--KYSFLQ-----N 48
 ||:| | : | :| ||||| | ||: |
 Db 3 FPSI-----FTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVL PFSN 57
 Qy 49 PLGTG-----PRFVNQHLCGSHLVEALYLVCGERGFFYTPKT-- 85
 | ||||| :
 Db 58 STNNGLLFINTTIIASIAAKEEGVSLDKRFVNQHLCGSHLVEALYLVCGERGFFYTPKSDD 117
 Qy 86 -RGIVEQCCTSICSLYQLENYCN 107
 :|||||||
 Db 118 AKGIVEQCCTSICSLYQLENYCN 140

RESULT 11

US-10-101-454-42

; Sequence 42, Application US/10101454

; Publication No. US20040110664A1

; GENERAL INFORMATION:

; APPLICANT: Havelund, Svend
 ; Halstrom, John
 ; Jonassen, Ib
 ; Andersen, Asser Sloth
 ; Markussen, Jan

; TITLE OF INVENTION: ACYLATED INSULIN

; NUMBER OF SEQUENCES: 49

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Novo Nordisk of North America, Inc.
 ; STREET: 405 Lexington Avenue, 64th Floor
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States of America
 ; ZIP: 10174-6401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/101,454
 ; FILING DATE: 20-Mar-2002
 ; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/400,256
 ; FILING DATE: 03-MAR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Lambiris, Elias J.
 ; REGISTRATION NUMBER: 33,728
 ; REFERENCE/DOCKET NUMBER: 3985.220-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-878-9655

; INFORMATION FOR SEQ ID NO: 42:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 140 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-101-454-42

Query Match 48.4%; Score 284; DB 16; Length 140;
Best Local Similarity 47.6%; Pred. No. 3.4e-25;
Matches 68; Conservative 6; Mismatches 27; Indels 42; Gaps 5;

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Qy      2 FPTIPLSRLFDNAMLRAHRLHQLAFDITYQEFEEAYIPKEQ--KYSFLQ-----N 48
      ||:|      |      :      |      :|      ||      ||      ||      ||      |
Db      3 FPSI-----FTAVLFAASSALAAPVNTTTTDETAQIPAEAVIGYSDLGDFDVAVLPPFSN 57

Qy      49 PLGTG-----PRFVNQHLCGSHLVEALYLVCGERGFFYTPKT-- 85
      |      |      |      |      |      |      |      |      |      |      |
Db      58 STNNGLLFINTTIIASIAAKEEGVSMARFVNQHLCGSHLVEALYLVCGERGFFYTPKSDD 117

Qy      86 -RGIVEQCCTSICSLYQLENYCN 107
      :|||||||||||||||||||||
Db     118 AKGIVEQCCTSICSLYQLENYCN 140
```

RESULT 12

US-10-101-454-15

; Sequence 15, Application US/10101454

; Publication No. US20040110664A1

; GENERAL INFORMATION:

; APPLICANT: Havelund, Svend
; Halstrom, John
; Jonassen, Ib
; Andersen, Asser Sloth
; Markussen, Jan

; TITLE OF INVENTION: ACYLATED INSULIN

; NUMBER OF SEQUENCES: 49

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/101,454
; FILING DATE: 20-Mar-2002
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/400,256
; FILING DATE: 03-MAR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3985.220-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-867-0123

; TELEFAX: 212-878-9655
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 104 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
 US-10-101-454-15

Query Match 47.9%; Score 281; DB 16; Length 104;
 Best Local Similarity 71.8%; Pred. No. 5.3e-25;
 Matches 56; Conservative 6; Mismatches 8; Indels 8; Gaps 3;

Qy 37 IPKEQ----KYSFLQNPLGTGPRFVNQHLGSHLVEALYLVCGERGFFYTPKT---RGIV 89
 ||:| : : | | : ||||| : : |||
 Db 28 IPEESLIIAENTTLAN-VAMAKRFVNQHLGSHLVEALYLVCGERGFFYTPKSDDAKGIV 86
 Qy 90 EQCCTSICSLYQLENYCN 107
 |||||
 Db 87 EQCCTSICSLYQLENYCN 104

RESULT 13

US-09-858-935B-5

; Sequence 5, Application US/09858935B
 ; Publication No. US20030069177A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dubaquié, Yves
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Lowman, Henry B.
 ; TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
 ; FILE REFERENCE: P1794R1
 ; CURRENT APPLICATION NUMBER: US/09/858,935B
 ; CURRENT FILING DATE: 2002-07-02
 ; PRIOR APPLICATION NUMBER: US 60/248,985
 ; PRIOR FILING DATE: 2000-11-15
 ; PRIOR APPLICATION NUMBER: US 60/204,490
 ; PRIOR FILING DATE: 2000-05-16
 ; NUMBER OF SEQ ID NOS: 153
 ; SEQ ID NO 5
 ; LENGTH: 51
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-858-935B-5

Query Match 47.4%; Score 278.5; DB 10; Length 51;
 Best Local Similarity 98.1%; Pred. No. 4.4e-25;
 Matches 51; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 56 FVNQHLGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
 |||||
 Db 1 FVNQHLGSHLVEALYLVCGERGFFYTPKT-GIVEQCCTSICSLYQLENYCN 51

RESULT 14

US-10-028-410-3

```
; Sequence 3, Application US/10028410
; Publication No. US20020160955A1
; GENERAL INFORMATION:
; APPLICANT: Dubaquier, Yves
; APPLICANT: Lowman, Henry
; TITLE OF INVENTION: PROTEIN VARIANTS
; FILE REFERENCE: P1712R1-1
; CURRENT APPLICATION NUMBER: US/10/028,410
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US/09/477,924
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 3
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-028-410-3
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```
Query Match          47.4%; Score 278.5; DB 13; Length 51;
Best Local Similarity 98.1%; Pred. No. 4.4e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
Qy      56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
          |||
Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKT-GIVEQCCTSICSLYQLENYCN 51
```

```
RESULT 15
US-10-444-326-3
; Sequence 3, Application US/10444326
; Publication No. US20030191065A1
; GENERAL INFORMATION:
; APPLICANT: Dubaquier, Yves
; APPLICANT: Lowman, Henry
; TITLE OF INVENTION: PROTEIN VARIANTS
; FILE REFERENCE: P1712R1
; CURRENT APPLICATION NUMBER: US/10/444,326
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US/09/723,866
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/477,923
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 3
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-444-326-3
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Query Match          47.4%; Score 278.5; DB 14; Length 51;
Best Local Similarity 98.1%; Pred. No. 4.4e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
Qy      56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
          |||
Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKT-GIVEQCCTSICSLYQLENYCN 51
```

Search completed: February 11, 2005, 19:03:53
Job time : 77.7823 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 11, 2005, 17:42:04 ; Search time 93.3782 Seconds
(without alignments)
586.780 Million cell updates/sec

Title: US-10-054-873-6
Perfect score: 587
Sequence: 1 MFPTIPLSRLFDNAMLRAHR.....IVEQCCTSICSLYQLENYCN 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	275	46.8	96	2	Q7MOU6	Q7m0u6 bacillus br
2	273.5	46.6	51	1	INS_BALPH	P67973 balaenopter
3	273.5	46.6	51	1	INS_ELEMA	P01316 elephas max
4	273.5	46.6	51	1	INS_PHYCA	P67974 physeter ca
5	273	46.5	110	1	INS_CERAE	P30407 cercopithec
6	273	46.5	110	1	INS_MACFA	P30406 macaca fasc
7	271.5	46.3	51	2	Q7M0G1	Q7m0g1 cricetidae
8	268.5	45.7	51	1	INS_ACOCA	P01324 acomys cahi
9	267.5	45.6	51	2	Q7M217	Q7m217 canavalia e
10	267	45.5	110	1	INS_GORGO	Q6yk33 gorilla gor
11	267	45.5	110	1	INS_HUMAN	P01308 homo sapien
12	267	45.5	110	1	INS_PANTR	P30410 pan troglod
13	267	45.5	110	1	INS_PONPY	Q8hxx2 pongo pygma
14	266	45.3	110	1	INS_SPETR	Q9lxi3 spermophilu
15	263.5	44.9	51	1	INS_BALBO	P01314 balaenopter

16	263.5	44.9	51	1	INS_CAMDR	P01320	camelus dro
17	263.5	44.9	51	1	INS_CAPHI	P01319	capra hircu
18	263	44.8	108	1	INS_PIG	P01315	sus scrofa
19	263	44.8	110	1	INS_RABIT	P01311	oryctolagus
20	262.5	44.7	51	1	INS_FELCA	P06306	felis silve
21	262	44.6	110	1	INS_CANFA	P01321	canis famil
22	261.5	44.5	51	1	INS_SAIISC	P67971	saimiri sci
23	260	44.3	110	1	INS_CRILO	P01313	cricetulus
24	258.5	44.0	105	1	INS_BOVIN	P01317	bos taurus
25	257	43.8	108	1	INS_AOTTR	P67972	aotus trivi
26	257	43.8	110	1	INS_PSAOB	Q62587	psammomys o
27	256.5	43.7	51	1	INS_DIDMA	P18109	didelphis m
28	255.5	43.5	217	1	SOMA_HUMAN	P01241	homo sapien
29	255.5	43.5	217	1	SOMA_MACMU	P33093	macaca mula
30	255.5	43.5	217	1	SOMA_PANTR	P58756	pan troglod
31	255.5	43.5	217	2	Q6IYF0	Q6iyf0	homo sapien
32	254.5	43.4	105	1	INS_SHEEP	P01318	ovis aries
33	252	42.9	86	1	INS_HORSE	P01310	equus cabal
34	251.5	42.8	51	1	INS_CHIBR	P01327	chinchilla
35	251.5	42.8	217	2	Q6IYF1	Q6iyf1	homo sapien
36	251	42.8	110	2	Q8WNW6	Q8wnw6	felis silve
37	250	42.6	108	1	INS1_MOUSE	P01325	mus musculu
38	249	42.4	110	1	INS1_RAT	P01322	rattus norv
39	249	42.4	217	1	SOMA_CALJA	Q9gmb3	callithrix
40	249	42.4	217	1	SOMA_SAIIB	P58343	saimiri bol
41	249	42.4	217	2	Q8WNE0	Q8wne0	ateles geof
42	248.5	42.3	51	1	INS_ANSAN	P68245	anser anser
43	248.5	42.3	51	1	INS_CAIMO	P68243	cairina mos
44	248	42.2	110	1	INS2_MOUSE	P01326	mus musculu
45	248	42.2	110	1	INS2_RAT	P01323	rattus norv

ALIGNMENTS

RESULT 1

Q7MOU6

ID Q7MOU6 PRELIMINARY; PRT; 96 AA.

AC Q7MOU6;

DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Epidermal growth factor/single chain insulin fusion protein

DE (Fragment).

OS Bacillus brevis (Brevibacillus brevis).

OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Brevibacillus.

OX NCBI_TaxID=1393;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20335834; PubMed=10879487;

RA Koh M., Hanagata H., Ebisu S., Morihara K., Takagi H.;

RT "Use of Bacillus brevis for synthesis and secretion of Des-B30 single-

RT chain human insulin precursor.";

RL Biosci. Biotechnol. Biochem. 64:1079-1081(2000).

DR PIR; PC7082; PC7082.

DR HSSP; P01308; 1EFE.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005179; F:hormone activity; IEA.
 DR GO; GO:0007582; P:physiological process; IEA.
 DR InterPro; IPR004825; Ins/IGF/relax.
 DR Pfam; PF00049; Insulin; 1.
 DR PRINTS; PR00277; INSULINB.
 DR PROSITE; PS00262; INSULIN; 1.
 FT NON_TER 1 1
 FT NON_TER 96 96
 SQ SEQUENCE 96 AA; 10473 MW; 4505D710C289092A CRC64;

Query Match 46.8%; Score 275; DB 2; Length 96;
 Best Local Similarity 94.3%; Pred. No. 5e-21;
 Matches 50; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

Qy 55 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
 :|||||
 Db 46 KFVNQHLCGSHLVEALYLVCGERGFFYTPK--GIVEQCCTSICSLYQLENYCN 96

RESULT 2

INS_BALPH

ID INS_BALPH STANDARD; PRT; 51 AA.
 AC P67973; P01312;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Insulin.
 GN Name=INS;
 OS Balaenoptera physalus (Finback whale) (Common rorqual).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
 OC Balaenopteridae; Balaenoptera.
 OX NCBI_TaxID=9770;
 RN [1]
 RP SEQUENCE.
 RX PubMed=14228503;
 RA Hama H., Titani K., Sakaki S., Narita K.;
 RT "The amino acid sequence in fin-whale insulin."
 RL J. Biochem. 56:285-293(1964).
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 CC increases cell permeability to monosaccharides, amino acids and
 CC fatty acids. It accelerates glycolysis, the pentose phosphate
 CC cycle, and glycogen synthesis in liver.
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 CC disulfide bonds.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the insulin family.
 DR PIR; A91918; INWHF.
 DR HSSP; P01317; 1APH.
 DR InterPro; IPR004825; Ins/IGF/relax.
 DR PRINTS; PR00277; INSULINB.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Direct protein sequencing; Glucose metabolism; Hormone;
 KW Insulin family.
 FT CHAIN 1 30 Insulin B chain.
 FT NON_CONS 30 31

FT CHAIN 31 51 Insulin A chain.
 FT DISULFID 7 37 Interchain.
 FT DISULFID 19 50 Interchain.
 FT DISULFID 36 41
 SQ SEQUENCE 51 AA; 5766 MW; 9007B514691A7CDD CRC64;

Query Match 46.6%; Score 273.5; DB 1; Length 51;
 Best Local Similarity 96.2%; Pred. No. 3.8e-21;
 Matches 50; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
 |||||||||||||||||||||||||||| ||||||||||||||||||||
 Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKA-GIVEQCCTSICSLYQLENYCN 51

RESULT 3

INS_ELEMA

ID INS_ELEMA STANDARD; PRT; 51 AA.

AC P01316;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Insulin.

GN Name=INS;

OS Elephas maximus (Indian elephant).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Proboscidea; Elephantidae; Elephas.

OX NCBI_TaxID=9783;

RN [1]

RP SEQUENCE.

RX MEDLINE=66160119; PubMed=5949593; DOI=10.1016/0002-9343(66)90145-8;

RA Smith L.F.;

RT "Species variation in the amino acid sequence of insulin.";

RL Am. J. Med. 40:662-666(1966).

CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 CC increases cell permeability to monosaccharides, amino acids and
 CC fatty acids. It accelerates glycolysis, the pentose phosphate
 CC cycle, and glycogen synthesis in liver.

CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 CC disulfide bonds.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- MISCELLANEOUS: The species of elephant is not given, but it is
 CC most probably the indian elephant (*Elephas maximus*).

CC -!- SIMILARITY: Belongs to the insulin family.

DR HSSP; P01308; 1AI0.

DR InterPro; IPR004825; Ins/IGF/relax.

DR PRINTS; PR00277; INSULINB.

DR SMART; SM00078; IIGF; 1.

DR PROSITE; PS00262; INSULIN; 1.

KW Direct protein sequencing; Glucose metabolism; Hormone;

KW Insulin family.

FT CHAIN 1 30 Insulin B chain.

FT NON_CONS 30 31

FT CHAIN 31 51 Insulin A chain.

FT DISULFID 7 37 Interchain.

FT DISULFID 19 50 Interchain.

FT DISULFID 36 41

SQ SEQUENCE 51 AA; 5752 MW; 9007B50CDB457D6D CRC64;

Query Match 46.6%; Score 273.5; DB 1; Length 51;
Best Local Similarity 94.2%; Pred. No. 3.8e-21;
Matches 49; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
| | | | | : | | | | |
Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKT-GIVEQCCTGVCSLYQLENYCN 51

RESULT 4

INS_PHYCA

ID INS_PHYCA STANDARD; PRT; 51 AA.
AC P67974; P01312;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Insulin.
GN Name=INS;
OS Physeter catodon (Sperm whale) (Physeter macrocephalus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Physeteridae; Physeter.
OX NCBI_TaxID=9755;
RN [1]
RP SEQUENCE.
RX PubMed=13373434;
RA Harris J.I., Sanger F., Naughton M.A.;
RT "Species differences in insulin.";
RL Arch. Biochem. Biophys. 65:427-438(1956).
RN [2]
RP SEQUENCE.
RX PubMed=13552701;
RA Ishihara Y., Saito T., Ito Y., Fujino M.;
RT "Structure of sperm- and sei-whale insulins and their breakdown by
RT whale pepsin.";
RL Nature 181:1468-1469(1958).
CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
CC increases cell permeability to monosaccharides, amino acids and
CC fatty acids. It accelerates glycolysis, the pentose phosphate
CC cycle, and glycogen synthesis in liver.
CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
CC disulfide bonds.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the insulin family.
DR PIR; A93142; INWHP.
DR HSSP; P01317; 1APH.
DR InterPro; IPR004825; Ins/IGF/relax.
DR PRINTS; PR00277; INSULINB.
DR SMART; SM00078; IIGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Direct protein sequencing; Glucose metabolism; Hormone;
KW Insulin family.
FT CHAIN 1 30 Insulin B chain.
FT NON_CONS 30 31
FT CHAIN 31 51 Insulin A chain.

FT DISULFID 7 37 Interchain.
 FT DISULFID 19 50 Interchain.
 FT DISULFID 36 41
 SQ SEQUENCE 51 AA; 5766 MW; 9007B514691A7CDD CRC64;

Query Match 46.6%; Score 273.5; DB 1; Length 51;
 Best Local Similarity 96.2%; Pred. No. 3.8e-21;
 Matches 50; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
 |||
 Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKA-GIVEQCCTSICSLYQLENYCN 51

RESULT 5

INS_CERAE

ID INS_CERAE STANDARD; PRT; 110 AA.

AC P30407; P01309;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Insulin precursor.

GN Name=INS;

OS Cercopithecus aethiops (Green monkey) (Grivet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopithecinae; Cercopithecus.

OX NCBI_TaxID=9534;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92219953; PubMed=1560757;

RA Seino S., Bell G.I., Li W.;

RT "Sequences of primate insulin genes support the hypothesis of a slower
 rate of molecular evolution in humans and apes than in monkeys.";

RL Mol. Biol. Evol. 9:193-203(1992).

RN [2]

RP SEQUENCE OF 57-87.

RX MEDLINE=72258016; PubMed=4626369;

RA Peterson J.D., Nehrlich S., Oyer P.E., Steiner D.F.;

RT "Determination of the amino acid sequence of the monkey, sheep, and
 dog proinsulin C-peptides by a semi-micro Edman degradation
 procedure.";

RL J. Biol. Chem. 247:4866-4871(1972).

CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 increases cell permeability to monosaccharides, amino acids and
 fatty acids. It accelerates glycolysis, the pentose phosphate
 cycle, and glycogen synthesis in liver.

CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 disulfide bonds.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the insulin family.

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CC or send an email to license@isb-sib.ch).

```

DR      EMBL; X61092; CAA43405.1; -.
DR      PIR; B42179; B42179.
DR      HSSP; P01308; 1AI0.
DR      InterPro; IPR004825; Ins/IGF/relax.
DR      Pfam; PF00049; Insulin; 1.
DR      PRINTS; PR00277; INSULINB.
DR      ProDom; PD015667; Mollusc_ins; 1.
DR      SMART; SM00078; IIGF; 1.
DR      PROSITE; PS00262; INSULIN; 1.
KW      Direct protein sequencing; Glucose metabolism; Hormone;
KW      Insulin family; Signal.
FT      SIGNAL          1          24
FT      CHAIN           25          54      Insulin B chain.
FT      PROPEP          57          87      C peptide.
FT      CHAIN           90         110      Insulin A chain.
FT      DISULFID        31          96      Interchain.
FT      DISULFID        43         109      Interchain.
FT      DISULFID        95         100
SQ      SEQUENCE       110 AA;  12019 MW;  95A1F54BE7B247F9 CRC64;

```

Query Match 46.5%; Score 273; DB 1; Length 110;
Best Local Similarity 60.2%; Pred. No. 9.4e-21;
Matches 53; Conservative 0; Mismatches 1; Indels 34; Gaps 1;

```

Qy      54 PRFVNQHLCGSHLVEALYLVCGERGFFYTPKT----- 85
      | |||||||||||||||||||
Db      23 PAFVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDPQVGQVELGGGPGAGSLQPLAL 82

Qy      86 -----RGIVEQCCTSICSLYQLENYCN 107
      |||||||||||||||
Db      83 EGS LQKRGIVEQCCTSICSLYQLENYCN 110

```

RESULT 6

INS MACFA

ID INS MACFA STANDARD; PRT; 110 AA.

AC P30406; P01309;

DT 21-JUL-1986 (Rel. 01, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Insulin precursor.

```
GN      Name=INS;
```

OS *Macaca fascicularis* (Crab eating macaque) (*Cynomolgus* monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopithecinae; Macaca.

OX NCBI TaxID=9541;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83080474; PubMed=6184262; DOI=10.1016/0378-1119(82)90004-X;

RA Wetekam W., Groneberg J., Leineweber M., Wengenmayer F.,

RA Winnacker E.-L.;

RT "The nucleotide sequence of cDNA coding for preproinsulin from the
RT primate *Macaca fascicularis*.";

RL Gene 19:179-183(1982).
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 CC increases cell permeability to monosaccharides, amino acids and
 CC fatty acids. It accelerates glycolysis, the pentose phosphate
 CC cycle, and glycogen synthesis in liver.
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 CC disulfide bonds.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the insulin family.
 CC -----
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 CC -----
 DR EMBL; J00336; AAA36849.1; -.
 DR PIR; JQ0178; JQ0178.
 DR HSSP; P01308; 1AI0.
 DR InterPro; IPR004825; Ins/IGF/relax.
 DR Pfam; PF00049; Insulin; 1.
 DR PRINTS; PR00277; INSULINB.
 DR ProDom; PD015667; Mollusc_ins; 1.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Glucose metabolism; Hormone; Insulin family; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 54 Insulin B chain.
 FT PROPEP 57 87 C peptide.
 FT CHAIN 90 110 Insulin A chain.
 FT DISULFID 31 96 Interchain.
 FT DISULFID 43 109 Interchain.
 FT DISULFID 95 100
 SQ SEQUENCE 110 AA; 11991 MW; 83C6E33A80A420F9 CRC64;

Query Match 46.5%; Score 273; DB 1; Length 110;
 Best Local Similarity 60.2%; Pred. No. 9.4e-21;
 Matches 53; Conservative 0; Mismatches 1; Indels 34; Gaps 1;

Qy 54 PRFVNQHLCGSHLVEALYLVCGERGFFYTPKT----- 85
 | |||||
 Db 23 PAFVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDPQVGQVELGGGPGAGSLQPLAL 82
 Qy 86 -----RGIVEQCCTSICSLYQLENYCN 107
 |||||
 Db 83 EGSLQKRGIVEQCCTSICSLYQLENYCN 110

RESULT 7

Q7M0G1

ID Q7M0G1 PRELIMINARY; PRT; 51 AA.
 AC Q7M0G1;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Insulin.
 OS Cricetidae sp. (Hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae.
 OX NCBI_TaxID=36483;
 RN [1]
 RP SEQUENCE.
 RA Neelon F.A., Delcher H.K., Steinman H., Lebovitz H.E.;
 RT "Structure of hamster insulin: comparison with a tumor insulin."
 RL Fed. Proc. 32:300-300(1973).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- SIMILARITY: Belongs to the insulin family.
 DR PIR; A91456; A91456.
 DR HSSP; P01308; 1EV6.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR GO; GO:0007582; P:physiological process; IEA.
 DR InterPro; IPR004825; Ins/IGF/relax.
 DR Pfam; PF00049; Insulin; 1.
 DR PRINTS; PR00277; INSULINB.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Insulin family.
 SQ SEQUENCE 51 AA; 5768 MW; 90066E6469047D3D CRC64;

Query Match 46.3%; Score 271.5; DB 2; Length 51;
 Best Local Similarity 94.2%; Pred. No. 6.1e-21;
 Matches 49; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSIICSLYQLENYCN 107
 |||||:|||||
 Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKS-GIVDQCCTSIICSLYQLENYCN 51

RESULT 8

INS_ACOCA

ID INS_ACOCA STANDARD; PRT; 51 AA.
 AC P01324;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Insulin.
 GN Name=INS;
 OS Acomys cahirinus (Egyptian spiny mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Acomys.
 OX NCBI_TaxID=10068;
 RN [1]
 RP PRELIMINARY SEQUENCE.
 RX MEDLINE=72189454; PubMed=5028210;
 RA Buenzli H.F., Humbel R.E.;
 RT "Isolation and partial structural analysis of insulin from mouse (Mus musculus) and spiny mouse (Acomys cahirinus).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:444-450(1972).
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 CC increases cell permeability to monosaccharides, amino acids and
 CC fatty acids. It accelerates glycolysis, the pentose phosphate
 CC cycle, and glycogen synthesis in liver.

CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 CC disulfide bonds.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the insulin family.
 DR PIR; A01591; INMSSP.
 DR HSSP; P01308; 1EV6.
 DR InterPro; IPR004825; Ins/IGF/relax.
 DR PRINTS; PR00277; INSULINB.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Direct protein sequencing; Glucose metabolism; Hormone;
 KW Insulin family.
 FT CHAIN 1 30 Insulin B chain.
 FT NON_CONS 30 31
 FT CHAIN 31 51 Insulin A chain.
 FT DISULFID 7 37 Interchain (By similarity).
 FT DISULFID 19 50 Interchain (By similarity).
 FT DISULFID 36 41 By similarity.
 SQ SEQUENCE 51 AA; 5768 MW; 992BD8B629047D3D CRC64;

Query Match 45.7%; Score 268.5; DB 1; Length 51;
 Best Local Similarity 92.3%; Pred. No. 1.3e-20;
 Matches 48; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy 56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
 ||:|||||||||||||||||||||||: ||:|||||||||||||||
 Db 1 FVBQHLCGSHLVEALYLVCGERGFFYTPKS-GIVDQCCTSICSLYQLENYCN 51

RESULT 9

Q7M217

ID Q7M217 PRELIMINARY; PRT; 51 AA.
 AC Q7M217;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Insulin precursor (Fragments).
 OS Canavalia ensiformis (Jack bean) (Horse bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Canavalia.
 OX NCBI_TaxID=3823;
 RN [1]
 RP SEQUENCE.
 RA Oliveira A.E.A., Machado O.L.T., Gomes V.M., Xavier-Neto J.,
 RA Pereira A.C.P., Vieira J.G.H., Fernandes K.V.S., Xavier-Filho J.;
 RT "Jack bean seed coat contains a protein with complete sequence
 RT homology to bovine insulin.";
 RL Protein Pept. Lett. 6:15-21(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- SIMILARITY: Belongs to the insulin family.
 DR PIR; B59151; B59151.
 DR HSSP; P01317; 1APH.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR GO; GO:0007582; P:physiological process; IEA.
 DR InterPro; IPR004825; Ins/IGF/relax.

DR PRINTS; PR00277; INSULINB.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Insulin family.
 FT NON_TER 1 1
 FT NON_TER 51 51
 SQ SEQUENCE 51 AA; 5722 MW; 9007B50CCA0A7DDD CRC64;

Query Match 45.6%; Score 267.5; DB 2; Length 51;
 Best Local Similarity 92.3%; Pred. No. 1.6e-20;
 Matches 48; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSIQSLYQLENYCN 107
 ||||| :|||
 Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKA-GIVEQCCASVCSLYQLENYCN 51

RESULT 10

INS_GORGO

ID INS_GORGO STANDARD; PRT; 110 AA.

AC Q6YK33;

DT 25-OCT-2004 (Rel. 45, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Insulin precursor.

GN Name=INS;

OS Gorilla gorilla gorilla (Lowland gorilla).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.

OX NCBI_TaxID=9595;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22833521; PubMed=12952878; DOI=10.1101/gr.948003;

RA Stead J.D.H., Hurles M.E., Jeffreys A.J.;

RT "Global haplotype diversity in the human insulin gene region.";

RL Genome Res. 13:2101-2111(2003).

CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 CC increases cell permeability to monosaccharides, amino acids and
 CC fatty acids. It accelerates glycolysis, the pentose phosphate
 CC cycle, and glycogen synthesis in liver.

CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 CC disulfide bonds.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the insulin family.

CC -----
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 CC -----

DR EMBL; AY137500; AAN06935.1; -.

DR InterPro; IPR004825; Ins/IGF/relax.

DR InterPro; IPR003234; Mollusc_ins.

DR Pfam; PF00049; Insulin; 1.

DR PRINTS; PR00277; INSULINB.

DR ProDom; PD015667; Mollusc_ins; 1.
 DR SMART; SM00078; ILGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Glucose metabolism; Hormone; Insulin family; Signal.
 FT SIGNAL 1 24 By similarity.
 FT CHAIN 25 54 Insulin B chain.
 FT PROPEP 57 87 C peptide.
 FT CHAIN 90 110 Insulin A chain.
 FT DISULFID 31 96 Interchain (By similarity).
 FT DISULFID 43 109 Interchain (By similarity).
 FT DISULFID 95 100 By similarity.
 SQ SEQUENCE 110 AA; 11981 MW; C2C3B23B85E520E5 CRC64;

Query Match 45.5%; Score 267; DB 1; Length 110;
 Best Local Similarity 60.5%; Pred. No. 4e-20;
 Matches 52; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

QY 56 FVNQHLCGSHLVEALYLVCGERGFFYTPKT----- 85
 ||||||||||||||||||||||||||||
 Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84
 QY 86 ----RGIVEQCCTSICSLYQLENYCN 107
 ||||||||||||||||||||
 Db 85 SLQKRGIVEQCCTSICSLYQLENYCN 110

RESULT 11

INS_HUMAN

ID INS_HUMAN STANDARD; PRT; 110 AA.
 AC P01308;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Insulin precursor.
 GN Name=INS;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80120725; PubMed=6243748;
 RA Bell G.I., Pictet R.L., Rutter W.J., Cordell B., Tischer E.,
 RA Goodman H.M.;
 RT "Sequence of the human insulin gene."
 RL Nature 284:26-32(1980).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80236313; PubMed=6248962;
 RA Ullrich A., Dull T.J., Gray A., Brosius J., Sures I.;
 RT "Genetic variation in the human insulin gene."
 RL Science 209:612-615(1980).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80054779; PubMed=503234;
 RA Bell G.I., Swain W.F., Pictet R.L., Cordell B., Goodman H.M.,
 RA Rutter W.J.;

RT "Nucleotide sequence of a cDNA clone encoding human preproinsulin."
 RL Nature 282:525-527(1979).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80147417; PubMed=6927840;
 RA Sures I., Goeddel D.V., Gray A., Ullrich A.;
 RT "Nucleotide sequence of human preproinsulin complementary DNA."
 RL Science 208:57-59(1980).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93364428; PubMed=8358440;
 RA Lucassen A.M., Bell J.I., Julier C., Lathrop M.;
 RT "Susceptibility to insulin dependent diabetes mellitus maps to a 4.1
 kb segment of DNA spanning the insulin gene and associated VNTR."
 RL Nat. Genet. 4:305-310(1993).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP SEQUENCE OF 1-59 FROM N.A.
 RC TISSUE=Blood;
 RA Fajardy I.I., Weill J.J., Stuckens C.C., Danze P.M.P.;
 RT "Description of a novel RFLP diallelic polymorphism (-127 BsgI C/G)
 within the 5' region of insulin gene."
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
 RN [8]
 RP SEQUENCE OF 25-54 AND 90-110.
 RX PubMed=14426955;
 RA Nicol D.S.H.W., Smith L.F.;
 RT "Amino-acid sequence of human insulin."
 RL Nature 187:483-485(1960).
 RN [9]
 RP SEQUENCE OF 57-87.
 RX MEDLINE=71116410; PubMed=5101771;
 RA Oyer P.E., Cho S., Peterson J.D., Steiner D.F.;
 RT "Studies on human proinsulin. Isolation and amino acid sequence of the

RT human pancreatic C-peptide."
 RL J. Biol. Chem. 246:1375-1386(1971).
 RN [10]
 RP SEQUENCE OF 57-87.
 RX MEDLINE=71257722; PubMed=5560404;
 RA Ko A., Smyth D.G., Markussen J., Sundby F.;
 RT "The amino acid sequence of the C-peptide of human proinsulin."
 RL Eur. J. Biochem. 20:190-199(1971).
 RN [11]
 RP SYNTHESIS.
 RX MEDLINE=75077277; PubMed=4443293;
 RA Sieber P., Kamber B., Hartmann A., Joehl A., Riniker B., Rittel W.;
 RT "Total synthesis of human insulin under directed formation of the
 RT disulfide bonds."
 RL Helv. Chim. Acta 57:2617-2621(1974).
 RN [12]
 RP SYNTHESIS OF 57-87.
 RX MEDLINE=75040007; PubMed=4803504;
 RA Naithani V.K.;
 RT "Studies on polypeptides, IV. The synthesis of C-peptide of human
 RT proinsulin."
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:659-672(1973).
 RN [13]
 RP SYNTHESIS OF 65-69 AND 70-73.
 RX MEDLINE=73161263; PubMed=4698555;
 RA Geiger R., Volk A.;
 RT "Synthesis of peptides with the properties of human proinsulin C
 RT peptides (hC peptide). 3. Synthesis of the sequences 14-17 and 9-13 of
 RT human proinsulin C peptides."
 RL Chem. Ber. 106:199-205(1973).
 RN [14]
 RP SYNTHESIS OF 84-87.
 RX MEDLINE=73161261; PubMed=4698553;
 RA Geiger R., Jaeger G., Keonig W., Treuth G.;
 RT "Synthesis of peptides with the properties of human proinsulin C
 RT peptides (hC peptide). I. Scheme for the synthesis and preparation of
 RT the sequence 28-31 of human proinsulin C peptide."
 RL Chem. Ber. 106:188-192(1973).
 RN [15]
 RP VARIANT LOS ANGELES SER-48.
 RX MEDLINE=84016053; PubMed=6312455;
 RA Haneda M., Chan S.J., Kwok S.C.M., Rubenstein A.H., Steiner D.F.;
 RT "Studies on mutant human insulin genes: identification and sequence
 RT analysis of a gene encoding [SerB24]insulin."
 RL Proc. Natl. Acad. Sci. U.S.A. 80:6366-6370(1983).
 RN [16]
 RP VARIANTS LOS ANGELES SER-48 AND CHICAGO LEU-49.
 RX MEDLINE=84170233; PubMed=6424111;
 RA Shoelson S., Fickova M., Haneda M., Nahum A., Musso G., Kaiser E.T.,
 RA Rubenstein A.H., Tager H.;
 RT "Identification of a mutant human insulin predicted to contain a
 RT serine-for-phenylalanine substitution."
 RL Proc. Natl. Acad. Sci. U.S.A. 80:7390-7394(1983).
 RN [17]
 RP VARIANT PROVIDENCE ASP-34.
 RX MEDLINE=87175640; PubMed=3470784;
 RA Chan S.J., Seino S., Gruppuso P.A., Schwartz R., Steiner D.F.;

RT "A mutation in the B chain coding region is associated with impaired
 RT proinsulin conversion in a family with hyperproinsulinemia.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:2194-2197(1987).
 RN [18]
 RP VARIANT WAKAYAMA LEU-92.
 RX MEDLINE=87058122; PubMed=3537011;
 RA Sakura H., Iwamoto Y., Sakamoto Y., Kuzuya T., Hirata H.;
 RT "Structurally abnormal insulin in a diabetic patient. Characterization
 RT of the mutant insulin A3 (Val-->Leu) isolated from the pancreas.";
 RL J. Clin. Invest. 78:1666-1672(1986).
 RN [19]
 RP VARIANT HIS-89.
 RX MEDLINE=90317021; PubMed=2196279;
 RA Barbetti F., Raben N., Kadowaki T., Cama A., Accili D., Gabbay K.H.,
 RA Merenich J.A., Taylor S.I., Roth J.;
 RT "Two unrelated patients with familial hyperproinsulinemia due to a
 RT mutation substituting histidine for arginine at position 65 in the
 RT proinsulin molecule: identification of the mutation by direct
 RT sequencing of genomic deoxyribonucleic acid amplified by polymerase
 RT chain reaction.";
 RL J. Clin. Endocrinol. Metab. 71:164-169(1990).
 RN [20]
 RP VARIANT HIS-89.
 RX MEDLINE=85261996; PubMed=4019786;
 RA Shibasaki Y., Kawakami T., Kanazawa Y., Akanuma Y., Takaku F.;
 RT "Posttranslational cleavage of proinsulin is blocked by a point
 RT mutation in familial hyperproinsulinemia.";
 RL J. Clin. Invest. 76:378-380(1985).
 RN [21]
 RP VARIANT KYOTO LEU-89.
 RX MEDLINE=92291307; PubMed=1601997;
 RA Yano H., Kitano N., Morimoto M., Polonsky K.S., Imura H., Seino Y.;
 RT "A novel point mutation in the human insulin gene giving rise to
 RT hyperproinsulinemia (proinsulin Kyoto).";
 RL J. Clin. Invest. 89:1902-1907(1992).
 RN [22]
 RP STRUCTURE BY NMR.
 RX MEDLINE=91104966; PubMed=2271664;
 RA Hua Q.-X., Weiss M.A.;
 RT "Toward the solution structure of human insulin: sequential 2D 1H NMR
 RT assignment of a des-pentapeptide analogue and comparison with crystal
 RT structure.";
 RL Biochemistry 29:10545-10555(1990).
 RN [23]
 RP STRUCTURE BY NMR.
 RX MEDLINE=91242467; PubMed=2036420;
 RA Hua Q.-X., Weiss M.A.;
 RT "Comparative 2D NMR studies of human insulin and des-pentapeptide
 RT insulin: sequential resonance assignment and implications for protein
 RT dynamics and receptor recognition.";
 RL Biochemistry 30:5505-5515(1991).
 RN [24]
 RP STRUCTURE BY NMR.
 RX MEDLINE=91265527; PubMed=1646635; DOI=10.1016/0167-4838(91)90098-K;
 RA Hua Q.-X., Weiss M.A.;
 RT "Two-dimensional NMR studies of Des-(B26-B30)-insulin: sequence-
 RT specific resonance assignments and effects of solvent composition.";

Query Match 45.5%; Score 267; DB 1; Length 110;
 Best Local Similarity 60.5%; Pred. No. 4e-20;
 Matches 52; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

Qy 56 FVNQHLCGSHLVEALYLVCGERGFFYTPKT----- 85
 |||||
 Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84
 Qy 86 ----RGIVEQCCTSICSLYQLENYCN 107
 |||||
 Db 85 SLQKRGIVEQCCTSICSLYQLENYCN 110

RESULT 12

INS_PANTR

ID INS_PANTR STANDARD; PRT; 110 AA.

AC P30410;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Insulin precursor.

GN Name=INS;

OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

OX NCBI_TaxID=9598;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92219953; PubMed=1560757;

RA Seino S., Bell G.I., Li W.;

RT "Sequences of primate insulin genes support the hypothesis of a slower

RT rate of molecular evolution in humans and apes than in monkeys.";

RL Mol. Biol. Evol. 9:193-203(1992).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=22833521; PubMed=12952878; DOI=10.1101/gr.948003;

RA Stead J.D.H., Hurles M.E., Jeffreys A.J.;

RT "Global haplotype diversity in the human insulin gene region.";

RL Genome Res. 13:2101-2111(2003).

CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 CC increases cell permeability to monosaccharides, amino acids and
 CC fatty acids. It accelerates glycolysis, the pentose phosphate
 CC cycle, and glycogen synthesis in liver.

CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 CC disulfide bonds.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the insulin family.

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 CC -----

DR EMBL; X61089; CAA43403.1; -.
 DR EMBL; AY137497; AAN06933.1; -.
 DR PIR; A42179; A42179.
 DR HSSP; P01308; 1AI0.
 DR InterPro; IPR004825; Ins/IGF/relax.
 DR Pfam; PF00049; Insulin; 1.
 DR PRINTS; PR00277; INSULINB.
 DR ProDom; PD015667; Mollusc_ins; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Glucose metabolism; Hormone; Insulin family; Signal.
 FT SIGNAL 1 24 By similarity.
 FT CHAIN 25 54 Insulin B chain.
 FT PROPEP 57 87 C peptide.
 FT CHAIN 90 110 Insulin A chain.
 FT DISULFID 31 96 Interchain (By similarity).
 FT DISULFID 43 109 Interchain (By similarity).
 FT DISULFID 95 100 By similarity.
 SQ SEQUENCE 110 AA; 12025 MW; 41EB8DF79837CEF5 CRC64;

Query Match 45.5%; Score 267; DB 1; Length 110;
 Best Local Similarity 60.5%; Pred. No. 4e-20;
 Matches 52; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

Qy 56 FVNQHLCGSHLVEALYLVCGERGFFYTPKT----- 85
 ||||||||||||||||||||||||||||
 Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84
 Qy 86 ----RGIVEQCCTSICSLYQLENYCN 107
 ||||||||||||||||||||
 Db 85 SLQKRGIVEQCCTSICSLYQLENYCN 110

RESULT 13

INS_PONPY

ID INS_PONPY STANDARD; PRT; 110 AA.

AC Q8HXV2;

DT 05-JUL-2004 (Rel. 44, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Insulin precursor.

GN Name=INS;

OS Pongo pygmaeus (Orangutan).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.

OX NCBI_TaxID=9600;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22833521; PubMed=12952878; DOI=10.1101/gr.948003;

RA Stead J.D.H., Hurles M.E., Jeffreys A.J.;

RT "Global haplotype diversity in the human insulin gene region.";

RL Genome Res. 13:2101-2111(2003).

CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 CC increases cell permeability to monosaccharides, amino acids and
 CC fatty acids. It accelerates glycolysis, the pentose phosphate
 CC cycle, and glycogen synthesis in liver.

CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 CC disulfide bonds.

```

CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: Belongs to the insulin family.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AY137503; AAN06937.1; -.
DR  HSSP; P01308; 1AI0.
DR  InterPro; IPR004825; Ins/IGF/relax.
DR  Pfam; PF00049; Insulin; 1.
DR  PRINTS; PR00277; INSULINB.
DR  ProDom; PD015667; Mollusc_ins; 1.
DR  SMART; SM00078; IIGF; 1.
DR  PROSITE; PS00262; INSULIN; 1.
KW  Glucose metabolism; Hormone; Insulin family; Signal.
FT  SIGNAL      1      24      By similarity.
FT  CHAIN       25     54      Insulin B chain.
FT  PROPEP      57     87      C peptide.
FT  CHAIN       90    110      Insulin A chain.
FT  DISULFID    31     96      Interchain (By similarity).
FT  DISULFID    43    109      Interchain (By similarity).
FT  DISULFID    95    100      By similarity.
SQ  SEQUENCE    110 AA;  12038 MW;  22D2B32B94F520F8 CRC64;

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Query Match          45.5%;  Score 267;  DB 1;  Length 110;
Best Local Similarity 60.5%;  Pred. No. 4e-20;
Matches 52;  Conservative 0;  Mismatches 0;  Indels 34;  Gaps 1;

```

```

Qy      56 FVNQHLCGSHLVEALYLVCGERGFFYTPKT----- 85
          |||
Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84
          |||
Qy      86 ----RGIVEQCCTSICSLYQLENYCN 107
          |||
Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110

```

RESULT 14

INS_SPETR

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ID  INS_SPETR      STANDARD;      PRT;    110 AA.
AC  Q91XI3;
DT  10-OCT-2003 (Rel. 42, Created)
DT  10-OCT-2003 (Rel. 42, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  Insulin precursor.
GN  Name=INS;
OS  Spermophilus tridecemlineatus (Thirteen-lined ground squirrel).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC  Spermophilus.
OX  NCBI_TaxID=43179;
RN  [1]

```

RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RA Tredrea M.M., Buck M.J., Guhaniyogi J., Squire T.L., Andrews M.T.;
 RT "Regulation of PDK4 expression in a hibernating mammal.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 CC increases cell permeability to monosaccharides, amino acids and
 CC fatty acids. It accelerates glycolysis, the pentose phosphate
 CC cycle, and glycogen synthesis in liver.
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 CC disulfide bonds.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the insulin family.
 CC -----
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 CC -----
 DR EMBL; AY038604; AAK72558.1; -.
 DR HSSP; P01308; 1EV6.
 DR InterPro; IPR004825; Ins/IGF/relax.
 DR Pfam; PF00049; Insulin; 1.
 DR PRINTS; PR00277; INSULINB.
 DR ProDom; PD015667; Mollusc_ins; 1.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Glucose metabolism; Hormone; Insulin family; Signal.
 FT SIGNAL 1 24 By similarity.
 FT CHAIN 25 54 Insulin B chain.
 FT PROPEP 57 87 C peptide.
 FT CHAIN 90 110 Insulin A chain.
 FT DISULFID 31 96 Interchain (By similarity).
 FT DISULFID 43 109 Interchain (By similarity).
 FT DISULFID 95 100 By similarity.
 SQ SEQUENCE 110 AA; 12004 MW; 4511768D6622BEE5 CRC64;

Query Match 45.3%; Score 266; DB 1; Length 110;
 Best Local Similarity 57.4%; Pred. No. 5.1e-20;
 Matches 54; Conservative 1; Mismatches 3; Indels 36; Gaps 2;

Qy 50 LGTGP--RFVNQHLCGSHLVEALYLVCGERGFFYTPKT----- 85
 || | |||||
 Db 17 LGPDPAQAFVNQHLCGSHLVEALYLVCGERGFFYTPKSRREVVEEQGGQVELGGPGAGL 76
 Qy 86 -----RGIVEQCCTSICSLYQLENYCN 107
 |||||
 Db 77 PQPLALEMALQKRGIVEQCCTSICSLYQLENYCN 110

RESULT 15

INS_BALBO

ID INS_BALBO STANDARD; PRT; 51 AA.

AC P01314;

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Insulin.
 GN Name=INS;
 OS Balaenoptera borealis (Sei whale).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
 OC Balaenopteridae; Balaenoptera.
 OX NCBI_TaxID=9768;
 RN [1]
 RP SEQUENCE.
 RX PubMed=13552701;
 RA Ishihara Y., Saito T., Ito Y., Fujino M.;
 RT "Structure of sperm- and sei-whale insulins and their breakdown by
 RT whale pepsin."
 RL Nature 181:1468-1469(1958).
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 CC increases cell permeability to monosaccharides, amino acids and
 CC fatty acids. It accelerates glycolysis, the pentose phosphate
 CC cycle, and glycogen synthesis in liver.
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 CC disulfide bonds.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the insulin family.
 DR PIR; A01582; INWH1S.
 DR HSSP; P01317; 1APH.
 DR InterPro; IPR004825; Ins/IGF/relax.
 DR PRINTS; PR00277; INSULINB.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Direct protein sequencing; Glucose metabolism; Hormone;
 KW Insulin family.
 FT CHAIN 1 30 Insulin B chain.
 FT NON_CONS 30 31
 FT CHAIN 31 51 Insulin A chain.
 FT DISULFID 7 37 Interchain.
 FT DISULFID 19 50 Interchain.
 FT DISULFID 36 41
 SQ SEQUENCE 51 AA; 5723 MW; 9007B50E400A7DDD CRC64;

Query Match 44.9%; Score 263.5; DB 1; Length 51;
 Best Local Similarity 92.3%; Pred. No. 4.2e-20;
 Matches 48; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
 |||||
 Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKA-GIVEQCCASTCSLYQLENYCN 51

Search completed: February 11, 2005, 18:22:49
 Job time : 93.3782 secs